(51) International Patent Classification: C12Q 1/68, A01K 67/02, C07K 14/65	A3	(11) International Publication Number: WO 00/36143
		(43) International Publication Date: 22 June 2000 (22.06.2000)

(54) Title: SELECTING ANIMALS FOR PARENTALLY IMPRINTED TRAITS
(54) Titre: SELECTION D'ANIMAUX EN FONCTION DE TRAITS COMMUNIQUES PAR LEURS PARENTS

(57) Abstract

The invention relates to methods to select breeding animals or animals destined for slaughter for having desired genotypic or potential phenotypic properties, in particular related to muscle mass and/or fat deposition. The invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a Sus scrofa chromosome 2 mapping at position 2p1.7.

(57) Abrégé

L'invention concerne des procédés de sélection d'animaux reproducteurs ou destinés à l'abattoir sur la base des propriétés génotypiques désirées ou des propriétés phénotypiques potentielles qui sont notamment liées à la masse musculaire et/ou aux dépôts de lard. L'invention se rapporte à un procédé pour sélectionner un porc possédant des propriétés génotypiques désirées ou des propriétés phénotypiques potentielles, ledit procédé consistant à tester un échantillon provenant dudit porc pour vérifier la présence d'un locus quantitatif (QTL) présent dans la cartographie de chromosome 2 de Sus scrofa en position 2p1.7.

PCT

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 : C12Q 1/68, C07K 14/65, A01K 67/02	A3	(11) International Publication Number: **WO 00/36143** (43) International Publication Date: 22 June 2000 (22.06.00)

(21) International Application Number: PCT/EP99/10209

(22) International Filing Date: 16 December 1999 (16.12.99)

(30) Priority Data:
98204291.3   16 December 1998 (16.12.98)   EP

(71) Applicants (for all designated States except US): UNIVER-SITY OF LIEGE [BE/BE]; 20 Bd de Colonster, B–4000 Liege (BE). MELICA HB [SE/SE]; Andersson, Leif, Bergagatan 30, S–752 39 Uppsala (SE). SEGHERSGENTEC N.V. [BE/BE]; Kapelbaan 15, B–9255 Buggenhout (BE).

(72) Inventors; and
(75) Inventors/Applicants (for US only): ANDERSSON, Leif [SE/SE]; Bergagatan 30, S–752 39 Uppsala (SE). GEORGES, Michel [BE/BE]; Rue Vieux Tige 24, B–3161 Villers–aux–Tours (BE). SPINCEMAILLE, Geert [BE/BE]; Sint Denijsstraat 26, B–8550 Zwevegem (BE).

(74) Agent: OTTEVANGERS, S., U.; Vereenigde, Nieuwe Parklaan 97, NL–2587 BN The Hague (NL).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

With international search report.

(88) Date of publication of the international search report:
26 October 2000 (26.10.00)

---

(54) Title: SELECTING ANIMALS FOR PARENTALLY IMPRINTED TRAITS

(57) Abstract

The invention relates to methods to select breeding animals or animals destined for slaughter for having desired genotypic or potential phenotypic properties, in particular related to muscle mass and/or fat deposition. The invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a Sus scrofa chromosome 2 mapping at position 2p1.7.

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7   C12Q1/68   C07K14/65   A01K67/02

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7   C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, CHEM ABS Data, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ANDERSSON-EKLUND ET AL.: "MAPPING QUANTITATIVE LOCI FOR CARCASS AND MEAT QUALITY TRAITS IN A WILD BOAR x LARGE WHITE INTERCROSS" J.ANIM.SCI., vol. 76, 1998, pages 694-700, XP002104406 cited in the application	1-3, 10-12
Y	See page 696, "Carcass Composition" and page 698, Fig. 1b. the whole document ---	4-9, 13-27

-/--

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
1 August 2000	08/08/2000

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Hagenmaier, S

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	KOVACS AND KLÖTING: "MAPPING OF QUANTITATIVE TRAIT LOCI FOR BODY WEIGHT ON CHROMOSOMS 1 AND 4 IN THE RAT" BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, vol. 44, no. 2, February 1998 (1998-02), pages 399-405, XP002104407	1,2,10, 11
Y	the whole document	4-9, 13-27
Y	JOHANSSON ET AL.: "COMPARATIVE MAPPING REVEALS EXTENSIVE LINKAGE CONSERVATION-BUT WITH GENE ORDER REARRAGEMENTS-BETWEEN THE PIG AND THE HUMAN GENOMES" GENOMICS, vol. 25, 1995, pages 682-690, XP000610181 See Fig.1, pig chromosome 2 the whole document	4-9, 13-27
Y	REIK W ET AL: "IMPRINTING IN CLUSTERS: LESSONS FROM BECKWITH-WIEDEMANN SYNDROME" TRENDS IN GENETICS, vol. 13, no. 8, 1 August 1997 (1997-08-01), page 330-334 XP004084608 Igf2 the whole document	4-9, 13-27
Y	CATCHPOLE AND ENGSTRÖM: "NUCLEOTIDE SEQUENCE OF A PORCINE INSULINE-LIKE GROWTH FACTOR II cDNA" NUCLEIC ACIDS RESEARCH, vol. 18, no. 21, 1990, page 6430 XP002104409 cited in the application the whole document	15
A	ANDERSSON L ET AL: "GENETIC MAPPING OF QUANTITATIVE TRAIT LOCI FOR GROWTH AND FATNESS IN PIGS" SCIENCE, vol. 263, 25 March 1994 (1994-03-25), pages 1771-1774, XP002018359 cited in the application the whole document	
A	KNOTT ET AL.: "MULTIPLE MARKER MAPPING OF QUANTITATIVE TRAIT LOCI IN A CROSS BETWEEN OUTBRED WILD BOAR AND LARGE WHITE PIGS" GENETICS, vol. 149, June 1998 (1998-06), pages 1069-1080, XP002104410 cited in the application the whole document	

-/--

1

Int. ..onal Application No

PCT/EP 99/10209

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
A	WO 98 03682 A (UNIV IOWA RES FOUND) 29 January 1998 (1998-01-29) the whole document	
P,X	JEON ET AL.: "A PATERNALLY EXPRESSED QTL AFFECTING SKELETAL AND CARDIAC MUSCLE MASS IN PIGS MAPS TO THE IGF2 LOCUS" NAT.GENET., vol. 21, February 1999 (1999-02), pages 157-158, XP002104411 the whole document	1-27
P,X	NEZER ET AL.: "AN IMPRINTED QTL WITH MAJOR EFFECT ON MUSCLE MASS AND FAT DEPOSITION MAPS TO THE IGF2 LOCUS IN PIGS" NAT.GENET., vol. 21, February 1999 (1999-02), pages 155-156, XP002104412 the whole document	1-27

Form PCT-ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 99/10209

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9803682	A	29-01-1998	US	5935784 A	10-08-1999
			AU	3513297 A	10-02-1998
			BR	9710875 A	11-01-2000
			CN	1230227 A	29-09-1999
			CZ	9900161 A	16-06-1999
			EP	0958376 A	24-11-1999
			PL	331353 A	05-07-1999
			US	5939264 A	17-08-1999

PCT

(51) International Patent Classification: C12Q 1/68, A01K 67/02, C07K 14/65	A2	(11) International Publication Number: WO 00/36143
		(43) International Publication Date: 22 June 2000 (22.06.2000)

(21) International Application Number: PCT/EP99/10209

(22) International Filing Date: 16 December 1999 (16.12.1999)

(30) Priority Data:
     98204291.3   16 December 1998 (16.12.1998) EP

(60) Parent Application or Grant
     UNIVERSITY OF LIEGE [/]; (). MELICA HB [/];
     (). SEGHERSGENTEC N.V. [/]; (). ANDERSSON, Leif [/];
     (). GEORGES, Michel [/]; (). SPINCEMAILLE, Geert [/];
     (). ANDERSSON, Leif [/]; (). GEORGES, Michel [/];
     (). SPINCEMAILLE, Geert [/]; (). OTTEVANGERS, S., U. ;
     ().

Published

(54) Title: SELECTING ANIMALS FOR PARENTALLY IMPRINTED TRAITS
(54) Titre: SELECTION D'ANIMAUX EN FONCTION DE TRAITS COMMUNIQUES PAR LEURS PARENTS

(57) Abstract

   The invention relates to methods to select breeding animals or animals destined for slaughter for having desired genotypic or potential phenotypic properties, in particular related to muscle mass and/or fat deposition. The invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a Sus scrofa chromosome 2 mapping at position 2p1.7.

(57) Abrégé

   L'invention concerne des procédés de sélection d'animaux reproducteurs ou destinés à l'abattoir sur la base des propriétés génotypiques désirées ou des propriétés phénotypiques potentielles qui sont notamment liées à la masse musculaire et/ou aux dépôts de lard. L'invention se rapporte à un procédé pour sélectionner un porc possédant des propriétés génotypiques désirées ou des propriétés phénotypiques potentielles, ledit procédé consistant à tester un échantillon provenant dudit porc pour vérifier la présence d'un locus quantitatif (QTL) présent dans la cartographie de chromosome 2 de Sus scrofa en position 2p1.7.

(54) Title: SELECTING ANIMALS FOR PARENTALLY IMPRINTED TRAITS

(57) Abstract

The invention relates to methods to select breeding animals or animals destined for slaughter for having desired genotypic or potential phenotypic properties, in particular related to muscle mass and/or fat deposition. The invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a Sus scrofa chromosome 2 mapping at position 2p1.7.

Description

5

10

15

20

25

30

35

40

45

50

55

Title: Selecting animals for parentally imprinted traits.

5

The invention relates to methods to select breeding
animals or animals destined for slaughter for having
desired genotypic or potential phenotypic properties, in
particular related to muscle mass and/or fat deposition.
10   Breeding schemes for domestic animals have so far focused
on farm performance traits and carcass quality. This has
resulted in substantial improvements in traits like
reproductive success, milk production, lean/fat ratio,
prolificacy, growth rate and feed efficiency. Relatively
15   simple performance test data have been the basis for
these improvements, and selected traits were assumed to
be influenced by a large number of genes, each of small
effect (the infinitesimal gene model). There are now some
important changes occurring in this area. First, the
20   breeding goal of some breeding organisations has begun to
include meat quality attributes in addition to the
"traditional" production traits. Secondly, evidence is
accumulating that current and new breeding goal traits
may involve relatively large effects (known as major
25   genes), as opposed to the infinitesimal model that has
been relied on so far.
       Modern DNA-technologies provide the opportunity to
exploit these major genes, and this approach is a very
promising route for the improvement of meat quality,
30   especially since direct meat quality assessment is not
viable for potential breeding animals. Also for other
traits such as lean/fat ratio, growth rate and feed
efficiency, modern DNA technology can be very effective.
Also these traits are not always easy to measure in the
35   living animal.
       The evidence for several of the major genes
originally obtained using segregation analysis, i.e.
without any DNA marker information. Afterwards molecular
studies were performed to detect the location of these

genes on the genetic map. In practice, and except for
alleles of very large effect, DNA studies are required to
dissect the genetic nature of most traits of economic
importance. DNA markers can be used to localise genes or
alleles responsible for qualitative traits like coat
colour, and they can also be used to detect genes or
alleles with substantial effects on quantitative traits
like growth rate, IMF etc. In this case the approach is
referred to as QTL (quantitative trait locus) mapping,
wherein a QTL comprises at least a part of the nucleic
acid genome of an animal where genetic information
capable of influencing said quantitative trait (in said
animal or in its offspring) is located. Information at
DNA level can not only help to fix a specific major gene
in a population, but also assist in the selection of a
quantitative trait which is already selected for.
Molecular information in addition to phenotypic data can
increase the accuracy of selection and therefore the
selection response.

Improving meat quality or carcass quality is not
just about changing levels of traits like tenderness or
marbling, but it is also about increasing uniformity. The
existence of major genes provides excellent opportunities
for improving meat quality because it allows large steps
to be made in the desired direction. Secondly, it will
help to reduce variation, since we can fix relevant genes
in our products. Another aspect is that selecting for
major genes allows differentiation for specific markets.
Studies are underway in several species, particularly,
pigs, sheep, deer and beef cattle.

In particular, intense selection for meat production
has resulted in animals with extreme muscularity and
leanness in several livestock species. In recent years it
has become feasible to map and clone several of the genes
causing these phenotypes, paving the way towards more
efficient marker assisted selection, targeted drug
development (performance enhancing products) and
transgenesis. Mutations in the ryanodine receptor (Fuji

et al, 1991; MacLennan and Phillips, 1993) and myostatin
(Grobet et al, 1997; Kambadur et al, 1997; McPherron and
Lee, 1997) have been shown to cause muscular
hypertrophies in pigs and cattle respectively, while

5   genes with major effects on muscularity and/or fat
deposition have for instance been mapped to pig
chromosome 4 (Andersson et al, 1994) and sheep chromosome
18 (Cocket et al, 1996).

However, although there have been successes in
10 identifying QTLs, the information is currently of limited
use within commercial breeding programmes. Many workers
in this field conclude that it is necessary to identify
the particular genes underlying the QTL. This is a
substantial task, as the QTL region is usually relatively
15 large and may contain many genes. Identification of the
relevant genes from the many that may be involved thus
remains a significant hurdle in farm animals.

The invention provides a method for selecting a
20 domestic animal for having desired genotypic or potential
phenotypic properties comprising testing said animal for
the presence of a parentally imprinted qualitative or
quantitative trait locus (QTL). Herein, a domestic animal
is defined as an animal being selected or having been
25 derived from an animal having been selected for having
desired genotypic or potential phenotypic properties.

Domestic animals provide a rich resource of genetic
and phenotypic variation, traditionally domestication
involves selecting an animal or its offspring for having
30 desired genotypic or potential phenotypic properties.
This selection process has in the past century been
facilitated by growing understanding and utilisation of
the laws of Mendelian inheritance. One of the major
problems in breeding programs of domestic animals is the
35 negative genetic correlation between reproductive
capacity and production traits. This is for example the
case in cattle (a high milk production generally results

in slim cows and bulls) poultry, broiler lines have a low
level of egg production and layers have generally very
low muscle growth), pigs (very prolific sows are in
general fat and have comparatively less meat) or sheep
5   (high prolific breeds have low carcass quality and vice
versa). The invention now provides that knowledge of the
parental imprinting character of various traits allows to
select for example sire lines homozygous for a paternally
imprinted QTL for example linked with muscle prcduction
10 or growth; the selection for such traits can thus be less
stringent in dam lines in favcur of the reproductive
quality. The phenomenon of genetic or parental imprinting
has never been utilised in selecting domestic animals, it
was never considered feasible to employ this elusive
15 genetic characteristic in practical breeding programmes.
The invention provides a breeding programme, wherein
knowledge of the parental imprinting character of a
desired trait, as demonstrated herein, results in a
breeding programme, for example in a BLUP programme, with
20 a modified animal model. This increases the accuracy of
the breeding value estimation and speeds up selection
compared to conventional breeding programmes. Until now,
the effect of a parentally imprinted trait in the
estimation of a conventional BLUP programme was
25 neglected; using and understanding the parental character
of the desired trait, as provided by the invention,
allows selecting on parental imprinting, even without DNA
testing. For example, selecting genes characterised by
paternal imprinting is provided to help increase
30 uniformity; a (terminal) parent homozygous for the "good
or wanted" alleles will pass them to all offspring,
regardless of the other parent's alleles, and the
offspring will all express the desired parent's alleles.
This results in more uniform offspring. Alleles that are
35 interesting or favourable from the maternal side or often
the ones that have opposite effects to alleles from the
paternal side. For example, in meat animals such as pigs
alleles linked with meat quality traits such as inta-

5

muscular fat or muscle mass could be fixed in the dam
lines while alleles linked with reduced back fat could be
fixed in the sire lines. Other desirable combinations are
for example fertility and/or milk yield in the female
5   line with growth rates and/or muscle mass in the male
lines.

In a preferred embodiment, the invention provides a
method for selecting a domestic animal for having desired
genotypic or potential phenotypic properties comprising
10   testing a nucleic acid sample from said animal for the
presence of a parentally imprinted quantitative trait
locus (QTL). A nucleic acid sample can in general be
obtained from various parts of the animal's body by
methods known in the art. Traditional samples for the
15   purpose of nucleic acid testing are blood samples or skin
or mucosal surface samples, but samples from other
tissues can be used as well, in particular sperm samples,
oocyte or embryo samples can be used. In such a sample,
the presence and/or sequence of a specific nucleic acid,
20   be it DNA or RNA, can be determined with methods known in
the art, such as hybridisation or nucleic acid
amplification or sequencing techniques known in the art.
The invention provides testing such a sample for the
presence of nucleic acid wherein a QTL or allele
25   associated therewith is associated with the phenomenon of
parental imprinting, for example where it is determined
whether a paternal or maternal allele of said QTL is
capable of being predominantly expressed in said animal.

The purpose of breeding programs in livestock is to
30   enhance the performances of animals by improving their
genetic composition. In essence this improvement accrues
by increasing the frequency of the most favourable
alleles for the genes influencing the performance
characteristics of interest. These genes are referred to
35   as QTL. Until the beginning of the nineties, genetic
improvement was achieved via the use of biometrical
methods, but without molecular knowledge of the
underlying QTL.

Since the beginning of the nineties and due to
recent developments in genomics, it is conceivable to
identify the QTL underlying a trait of interest. The
invention now provides identifying and using parentally
5   imprinted QTLs which are useful for selecting animals by
mapping quantitative trait loci. Again, the phenomenon of
genetic or paternal imprinting has never been utilised in
selecting domestic animals, it was never considered
feasible to employ this elusive genetic characteristic in
10   practical breeding programmes. For example Kovacs and
Kloting (Biochem. Mol. Biol. Int. 44:399-405, 1998),
where parental imprinting is not mentioned, and not
suggested, found linkage of a trait in female rats, but
not in males, suggesting a possible sex specificity
15   associated with a chromosomal region, which of course
excludes parental imprinting, a phenomenon wherein the
imprinted trait of one parent is preferably but gender-
aspecifically expressed in his or her offspring.

The invention provides the initial localisation of a
20   parentally imprinted QTL on the genome by linkage
analysis with genetic markers, and the actual
identification of the parentally imprinted gene(s) and
causal mutations therein. Molecular knowledge of such a
parentally imprinted QTL allows for more efficient
25   breeding designs herewith provided. Applications of
molecular knowledge of parentally imprinted QTLs in
breeding programs include: marker assisted segregation
analysis to identify the segregation of functionally
distinct parentally imprinted QTL alleles in the
30   populations of interest, marker assisted selection (MAS)
performed within lines to enhance genetic response by
increasing selection accuracy, selection intensity or by
reducing the generation interval using the understanding
of the phenomonon of parental imprinting, marker assisted
35   introgression (MAI) to efficiently transfer favourable
parentally imprinted QTL alleles from a donor to a
recipient population, genetic engineering of the
identified parentally QTL and genetic modification of the
breeding stock using transgenic technology, development

of performance enhancing products using targeted drug development exploiting molecular knowledge of said QTL.

The inventors undertook two independent experiments to determine the practical use of parental imprinting of a QTL.

In a first experiment, performed in a previously described Piétrain x Large White intercross, the likelihood of the data were computed under a model of paternal (paternal allele only expressed) and maternal imprinting (maternal allele only expressed) and compared with the likelihood of the data under a model of a conventional "Mendelian" QTL. The results strikingly demonstrated that the QTL was indeed paternally expressed, the QTL allele (Piétrain or Large White) inherited from the F1 sow having no effect whatsoever on the carcass quality and quantity of the F_2 offspring. It was seen that very significant lodscores were obtained when testing for the presence of a paternally expressed QTL, while there was no evidence at all for the segregation of a QTL when studying the chromosomes transmitted by the sows. The same tendency was observed for all traits showing that the same imprinted gene is responsible for the effects observed on the different traits. Table 1 reports the maximum likelihood (ML) phenotypic means for the F_2 offspring sorted by inherited paternal QTL allele.

In a second experiment performed in the Wild Boar X Large White intercross, QTL analyses of body composition, fatness, meat quality, and growth traits was carried out with the chromosome 2 map using a statistical model testing for the presence of an imprinting effect. Clear evidence for a paternally expressed QTL located at the very distal tip of 2p was obtained (Fig. 2; Table1). The clear paternal expression of a QTL is illustrated by the least squares means which fall into two classes following the population origin of the paternally inherited allele (Table 1). For a given paternally imprinted QTL, implementation of marker assisted segregation analysis, selection (MAS) and introgression (MAI), can be performed

using genetic markers that are linked to the QTL, genetic
markers that are in linkage disequilibrium with the QTL,
or using the actual causal mutations within the QTL.

5   Understanding the parent-of-origin effect
characterising a QTL allows for its optimal use in
breeding programs. Indeed, marker assisted segregation
analysis under a model of parental imprinting will yield
better estimates of QTL allele effects. Moreover it
allows for the application of specific breeding schemes
10   to optimally exploit a QTL. In one embodiment of the
invention, the most favourable QTL alleles would be fixed
in breeding animal lines and for example used to generate
commercial, crossbred males by marker assisted selection
(MAS, within lines) and marker assisted introgression
15   (MAI, between lines). In another embodiment, the worst
QTL alleles would be fixed in the animal lines used to
generate commercial crossbred females by MAS (within
lines) and MAI (between lines).

In a preferred embodiment of the invention, said
20   animal is a pig. Note for example that the invention
provides the insight that today half of the offspring
from commercially popular Piétrain$_x$ Large White crossbred
boars inherit an unfavourable Large White muscle mass QTL
as provided by the invention causing considerable loss,
25   and the invention now for example provides the
possibility to select the better half of the population
in that respect. However, it is also possible to select
commercial sow lines enriched with the in the boars
unfavourable alleles, allowing to equip the sows with
30   other alleles more desirable for for example reproductive
purposes.

In a preferred embodiment of a method provided by
the invention, said QTL is located at a position
corresponding to a QTL located at chromosome 2 in the
35   pig. For example, it is known form comparative mapping
data between pig and human, including bidirectional
chromosome painting, that SSC2p is homologous to
HSA11pter-q13[11,12]. HSA11pter-q13 is known to harbour a

cluster of imprinted genes: IGF2, INS2, H19, MAH2, P57^{KIP2},
K,LQTL1, Tapa1,/CD81, Orctl2, Impt1 and Ip1. The cluster
of imprinted genes located in HSA11pter-q13 is
characterised by 8 maternally expressed genes H19, MASH2,
5   P57^{KIP2}, K,LQTL1, TAPA1/CD81, ORCTL2, IMPT1 and IP1, and
two paternally expressed genes: IGF2 and INS. However,
Johanson et al (Genomics 25:682-690, 1995) and Reik et al
(Trends in Genetics, 13:330-334, 1997) show that the
whereabouts of these loci in various animals are not
10   clear. For example, the HSA11 and MMU7 loci do not
correspond among each other, the MMU7 and the SSC2 loci
do not correspond, whereas the HSA11 and SSC2 loci seem
to correspond, and no guidance is given where one or more
of for example the above identified parentally expressed
15   individual genes are localised on the three species'
chromosomes.

        Other domestic animals, such as cattle, sheep,
poultry and fish, having similar regions in their genome
harbouring such a cluster of imprinted genes or QTLs, the
20   invention herewith provides use of these orthologous
regions of other domestic animals in applying the
phenomenon of parental imprinting in breeding programmes.
In pigs, said cluster is mapped at around position 2p1.7
of chromosome 2, however, a method as provided by the
25   invention employing (fragments of) said maternally or
paternally expressed orthologous or homologous genes or
QTLs are advantageously used in other animals as well for
breeding and selecting purposes. For example, a method is
provided wherein said QTL is related to the potential
30   muscle mass and/or fat deposition, preferably with
limited effects on other traits such as meat quality and
daily gain of said animal or wherein said QTL comprises
at least a part of an insulin-like growth factor-2 (IGF2)
allele. Reik et al (Trends in Genetics, 13:330-334, 1997)
35   explain that this gene in humans is related to Beckwith-
Wiedemann syndrome, an apparently parentally imprinted
disease syndrome most commonly seen with human foetuses,
where the gene has an important role in prenatal

development. No relationship is shown or suggested with postnatal development relating to muscle development or fatness in (domestic) animals.

In a preferred embodiment, the invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a Sus scrofa chromosome 2 mapping at position 2p1.7. In particular, the invention relates to the use of genetic markers for the telomeric end of pig chromosome 2p in marker selection (MAS) of a parentally imprinted Quantitative Trait Locus (QTL) affecting carcass yield and quality in pigs. Furthermore, the invention relates to the use of genetic markers associated with the IGF2 locus in MAS in pigs, such as polymorphisms and microsatelites and other characterising nucleic acid sequences shown herein, such as shown in figures 4 to 10. In a preferred embodiment, the invention provides a QTL located at the distal tip of Sus scrofa chromosomes 2 with effects on varies measurements of carcass quality and quantity, particularly muscle mass and fat deposition.

In a first experiment, a QTL mapping analysis was performed in a Wild Boar X Large White intercross counting 200 F_2 individuals. The F_2 animals were sacrificed at a live eight of at least 60 kg or at a maximum age of 190 days. Phenotypic data on birth weight, growth, fat deposition, body composition, weight of internal organs, and meat quality were collected; a detailed description of the phenotypic traits are provided by Andersson et al[1] and Andersson-Eklund et al[4].

A QTL (without any significant effect on back-fat thickness) at an unspecified locus on the proximal end of chromosome 2 with moderate effect on muscle mass, and located about 30cM away from the parentally imprinted QTL reported here, was previously reported by the inventors; whereas the QTL as now provided has a very large effect, explaining at least 20-30% of variance, making the QTL of

the present invention commercially very attractive, which
is even more so because the present QTL is parentally
imprinted. The marker map of chromosome 2p was improved
as part of this invention by adding microsatellite
5   markers in order to cover the entire chromosome arm. The
following microsatellite markers were used: Swc9, Sw2443,
Sw2623, and Swr2516, all from the distal end of 2p[7]. QTL
analyses of body composition, fatness, meat quality, and
growth traits were carried out with the new chromosome 2
10 map. Clear evidence for a QTL located at the very distal
tip of 2p was obtained (Fig. 1; Table 1). The QTL had
very large effects on lean meat content in ham and
explained an astonishing 30% of the residual phenotypic
variance in the F_2 population. Large effects on the area
15 of the longissumus dorsi muscle, on the weight of the
heart, and on back-fat thickness (subcutaneous fat) were
also noted. A moderate effect on one meat quality trait,
reflectance value, was indicated. The QTL had no
significant effect on abdominal fat, birth weight,
20 growth, weight of liver, kidney, or spleen (data not
shown). The Large White allele at this QTL was associated
with larger muscle mass and reduced back-fat thickness
consistent with the difference between this breed and the
Wild Boar population.

25   In a second experiment, QTL mapping was performed in
a Piétrain X Large White intercross comprising 1125 F_2
offspring. The Large White and Piétrain parental breeds
differ for a number of economically important phenotypes.
Piétrains are famous for their exceptional muscularity
30 and leanness [10](Figure 2, while Large Whites show superior
growth performance. Twenty-one distinct phenotypes
measuring growth performance (5), muscularity (6), fat
deposition (6), and meat quality (4), were recorded on
all F_2 offspring. In order to map QTL underlying the
35 genetic differences between these breeds, the inventors
undertook a whole genome scan using microsatellite
markers on an initial sample of 677 F_2 individuals. The
following microsatellite marker map was used to analyse

chromosome 2;:SW2443, SWC9 and SW2623, SWR2516-(0,20)-

SWR783-(0,29)-SW240-(0,20)-SW776-(0,08)-S0010-(0,04)-

SW1695-(0,36)-SWR308. Analysis of pig chromosome 2 using

a Maximum Likelihood multipoint algorithm, revealed ·

5   highly significant lodscores (up to 20) for three of the

six phenotypes measuring muscularity (% lean cuts, % ham,

% loin) and three of the six phenotypes measuring fat

deposition (back-fat thickness (BFT), % backfat, % fat

cuts) at the distal end of the short arm of chromosome 2

10   (Figure 1). Positive lodscores were obtained in the

corresponding chromosome region for the remaining six

muscularity and fatness phenotypes, however, not reaching

the experiment-wise significance threshold) (α=5%. There

was no evidence for an effect of the corresponding QTL on

15· growth performance (including birth weight) or recorded

meat quality measurements (data not shown). To confirm

this finding, the remaining sample of 355 F_2 offspring was

genotyped for the four most distal 2p markers and QTL

analysis performed for the traits yielding the highest

20   lodscores in the first analysis. Lodscores ranged from

2.1 to 7.7, clearly confirming the presence of a major

QTL in this region. Table 2 reports the corresponding ML

estimates for the three genotypic means as well as the

residual variance. Evidence based on marker assisted

25   segregation analysis points towards residual segregation

at this locus within the Piétrain population.

These experiments therefore clearly indicated

the existence of a QTL with major effect on carcass

quality and quantity on the telomeric end of pig

30 . chromosome arm 2p; the likely existence of an allelic

series at this QTL with at least three alleles: Wild-Boar

< Large White < Piétrain, and possibly more given the

observed segregation within the Piétrain breed.

The effects of the identified QTL on muscle mass and

35   fat deposition are truly major, being of the same

magnitude of those reported for the CRC locus though ·

apparently without the associated deleterious effects on

meat quality. We estimate that both loci jointly explain

close to 50% of the Piétrain versus Large White breed
difference for muscularity and leanness. The QTL had very
large effects on lean meat content in ham and explained
an astonishing 30% of the residual phenotypic variance in
5   the F₂ population. Large effects on the area of the
longissumus dorsi muscle, on the weight of the heart, and
on back-fat thickness (subcutaneous fat) were also noted.
A moderate effect on one meat quality trait, reflectance
value, was indicated. The QTL had no significant effect
10   on abdominal fat, birth weight, growth, weight of liver,
kidney, or spleen (data not shown). The Large White
allele at this QTL, when compared to the Wild Boar
allele, was associated with larger muscle mass and
reduced back-fat thickness consistent with the difference
15   between this breed and the Wild Boar population. The
strong imprinting effect observed for all affected traits
shows that a single causative locus is involved. The
pleiotropic effects on skeletal muscle mass and the size
of the heart appear adaptive from a physiological point
20   of view as a larger muscle mass requires a larger cardiac
output.

        In a further embodiment, the invention provides a
method for selecting a pig for having desired genotypic
or potential phenotypic properties comprising testing a
25   sample from said pig for the presence of a quantitative
trait locus (QTL) located at a Sus scrofa chromosome 2
mapping at position 2p1.7., wherein said QTL comprises at
least a part of a Sus scrofa insulin-like growth factor-2
(IGF2) allele or a genonic area closely related thereto,
30   such as polymorphisms and microsatelites and other
characterising nucleic acid sequences shown herein, such
as shown in figures 4 to 10. The important role of IGF2
for prenatal development is well-documented from knock-
out mice as well as from its causative role in the human
35   Beckwith-Wiedemann syndrome. This invention demonstrates
an important role for the IGF2-region also for postnatal
development.

To show the role of Igf2 the inventors performed the following three experiments:

A genomic IGF2 clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone gave a strong consistent signal on the terminal part of chromosome 2p.

A polymorphic microsatellite is located in the 3'UTR of IGF2 in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible presence of a corresponding porcine microsatellite was investigated by direct sequencing of the IFG2 3'UTR using the BAC clone. A complex microsatellite was identified about 800bp downstream of the stop codon; a sequence comparison revealed that this microsatellite was identical to a previously described anonymous microsatellite, Swc9[6]. This marker was used in the initial QTL mapping experiments and its location on the genetic map correspond with the most likely position of the QTL both in the Piétrain X Large White and in the Large White x Wild Boar pedigree.

Analysis of skeletal muscle and liver cDNA from 10-week old foetuses heterozygous for a nt241 (G-A) transversion in the second exon of the porcine IGFII gene and SWC9, shows that the IGFII gene is imprinted in these tissues in the pig as well and only expressed from the paternal allele.

Based on a published porcine adult liver cDNA sequence[16], the inventors designed primer pairs allowing to amplify the entire IgfII coding sequence with 222 bp of leader and 280 bp of trailor sequence from adult skeletal muscle cDNA. Piétrain and Large White RT-PCR products were sequenced indication that the coding sequences are identical in both breeds and with the published sequence. However, a G⊗A transition was found in the leader sequence corresponding to exon 2 in man. Following conventional nomenclature, this polymorphism will be referred to as nt241(G-A). We developed a screening test for this single nucleotide polymorphism

9(SNP) based on the ligation amplification reaction
(LAR), allowing us to genotype our pedigree material.
Based on these data, *IgfII* was shown to colocalize with
the SWC9 microsatellite marker ($\theta=0\%$), therefore

5   virtually coinciding with the most likely position of the
QTL, and well within the 95% support interval for the
QTL. Subsequent sequence analysis demonstrated that the
microsatellite marker SWC9 is actually located within the
3'UTR of the *IgfII* gene.

10   As previously mentioned, the knowledge of this
QTL provides a method for the selection of animals such
as pigs with improved carcass merit. Different
embodiments of the invention are envisaged, including:
marker assisted segregation analysis to identify the

15   segregation of functionally distinct QTL alleles in the
populations of interest; marker assisted selection (MAS)
performed within lines to enhance genetic response by
increasing selection accuracy, selection intensity or by
reducing the generation interval; marker assisted

20   introgression (MAI) to efficiently transfer favourable
QTL alleles from a donor to a recipient population;
thereby enhancing genetic response in the recipient
population. Implementation of embodiments marker assisted
segregation analysis, selection (MAS) and introgression

25   (MAI), can be performed using genetic markers that are
linked to the QTL; genetic markers that are in linkage
disequilibrium with the QTL, the actual causal mutations
within the QTL.

         In a further embodiment, the invention provides a
30   method for selecting a pig for having desired genotypic
or potential phenotypic properties comprising testing a
sample from said pig for the presence of a quantitative
trait locus (QTL) located at a Sus scrofa chromosome 2
mapping at position 2p1.7., wherein said QTL is

35   paternally expressed, i.e. is expressed from the paternal
allele. In man and mouse, *Igf2* is known to be imprinted
and to be expressed exclusively from the paternal allele
in several tissues· Analysis of skeletal muscle cDNA from

pigs heterozygous for the SNP and/or SWC9, shows that the
same imprinting holds in the pig as well. Understanding
the parent-of-origin effect characterising the QTL as
provided by the invention now allows for its optimal use
5   in breeding programs. Indeed, today half of the offspring
from commercially popular Piétrain x Large White
crossbred boars inherit the unfavourable Large White
allele causing considerable loss. Using a method as
provide by the invention avoids this problem.
10   The invention furthermore provides an isolated
and/or recombinant nucleic acid or functional fragment
derived thereof comprising a parentally imprinted
quantitative trait locus (QTL) or fragment thereof
capable of being predominantly expressed by one parental
15   allele. Having such a nucleic acid as provided by the
invention available allows constructing transgenic
animals wherein favourable genes are capable of being
exclusively or predominantly expressed by one parental
allele, thereby equipping the offspring of said animal
20   homozygous for a desired trait with desired properties
related to that parental allele that is expressed.
         In a preferred embodiment, the invention provides an
isolated and/or recombinant nucleic acid or fragment
derived thereof comprising a synthetic parentally
25   imprinted quantitative trait locus (QTL) or functional
fragment thereof derived from at least one chromosome.
Synthetic herein describes a parentally expressed QTL
wherein various elements are combined that originate from
distinct locations from the genome of one or more
30   animals. The invention provides recombinant nucleic acid
wherein sequences related to parental imprinting of one
QTL are combined with sequences relating to genes or
favourable alleles of a second QTL. Such a gene construct
is favourably used to obtain transgenic animals wherein
35   the second QTL has been equipped with paternal
imprinting, as opposed to the inheritance pattern in the
native animal from which the second QTL is derived. Such
a second QTL can for example be derived from the same

chromosome where the parental imprinting region is
located, but can also be derived from a different
chromosome from the same or even a different species. In
the pig, such a second QTL can for example be related to

5   an oestrogen receptor (ESR)-gene (Rothschild et al, PNAS,
93, 201-201, 1996) or a FAT-QTL (Andersson, Science, 263,
1771-1774, 1994) for example derived from an other pig
chromosome, such as chromosome 4. A second or further QTL
can also be derived from another (domestic) animal or a

10   human.
        The invention furthermore provides an isolated
and/or recombinant nucleic acid or functional fragment
derived thereof at least partly corresponding to a QTL of
a pig located at a Sus scrofa chromosome 2 mapping at

15   position 2p1.7 wherein said QTL is related to the
potential muscle mass and/or fat deposition of said pig
and/or wherein said QTL comprises at least a part of a
Sus scrofa insulin-like growth factor-2 (IGF2) allele,
preferably at least spanning a region between INS and

20   H19, or preferably derived from a domestic pig, such as a
Pietrain, Meishan, Duroc, Landrace or Large White, or
from a Wild Boar. For example, a genomic IGF2 clone was
isolated by screening a porcine BAC library. FISH
analysis with this BAC clone gave a strong consistent

25   signal on the terminal part of chromosome 2p. A
polymorphic microsatellite is located in the 3'UTR of
IGF2 in mice (GenBank U71085), humans (GenBank S62623),
and horse (GenBank AF020598). The possible presence of a
corresponding porcine microsatellite was investigated by

30   direct sequencing of the IGF2 3'UTR using the BAC clone.
A complex microsatellite was identified about 800 bp
downstream of the stop codon; a sequence comparison
revealed that this microsatellite is identical to a
previously described anonymous microsatellite, Swc9. PCR

35   primers were designed and the microsatellite (IGF2ms) was
found to be highly polymorphic with three different
alleles among the two Wild Boar founders and another two

among the eight Large White founders. *IGF2ms* was fully
informative in the intercross as the breed of origin as
well as the parent of origin could be determined with
confidence for each allele in each F_2 animal.

A linkage analysis using the intercross pedigree was
carried out with *IGF2ms* and the microsatellites *Sw2443*,
Sw2623, and *Swr2516*, all from the distal end of 2p[7]. *IGF2*
was firmly assigned to 2p by highly significant lod
scores (e.g. Z=89.0, θ=0.003 against *Swr2516*). Multipoint
analyses, including previously typed chromosome 2
markers, revealed the following order of loci (sex-
average map distances in Kosambi cM): *Sw2443/Swr2516*-0.3-
IGF2-14.9-*Sw2623*-10.3-*Sw256*. No recombinant was observed
between *Sw2443* and *Swr2516*, and the suggested proximal
location of *IGF2* in relation to these loci is based on a
single recombinant giving a lod score support of 0.8 for
the reported order. The most distal marker in our
previous QTL study, *Sw256*, is located about 25 cM from
the distal end of the linkage group.

The invention furthermore provides use of a nucleic
acid or functional fragment derived thereof according to
the invention in a method according to the invention. In
a preferred embodiment, use of a method according to
invention is provided to select a breeding animal or
animal destined for slaughter, or embryos or semen
derived from these animals for having desired genotypic
or potential phenotypic properties. In particular, the
invention provides such use wherein said properties are
related to muscle mass and/or fat deposition. The QTL as
provided by the invention may be exploited or used to
improve for example lean meat content or back-fat
thickness by marker assisted selection within populations
or by marker assisted introgression of favorable alleles
from one population to another. Examples of marker
assisted selection using the QTL as provided by the
invention are use of marker assisted segregation analysis

with linked markers or with markers in disequilibrium to
identify functionally distinct QTL alleles. Furthermore,
identification of a causative mutation in the QTL is now
possible, again leading to identify functionally distinct
5   QTL alleles. Such functionally distinct QTL alleles
located at the distal tip of chromosome 2p with large
effects on skeletal muscle mass, the size of the heart,
and on back-fat thickness are also provided by the
invention. The observation of a similar QTL effect in a
10   Large White x Wild Boar as well as in a Piétrain x Large
White intercross provides proof of the existence of a
series of at least three distinct functional alleles.
Moreover, preliminary evidence based on marker assisted
segregation analysis points towards residual segregation
15   at this locus within the Piétrain population (data not
shown). The occurrence of an allelic series as provided
by the invention allows identifying causal polymorphisms
which - based on the quantitative nature of the observed
effect - are unlikely to be gross gene alterations but
20   rather subtle regulatory mutations. The effects on muscle
mass of the three alleles rank in the same order as the
breeds in which they are found i.e. Piétrain pigs are
more muscular than Large White pigs that in turn have
higher lean meat content than Wild Boars. The invention
25   furthermore provides use of the alleles as provided by
the invention for within line selection or for marker
assisted introgression using linked markers, markers in
disequilibrium or alleles comprising causative mutations.
     The invention furthermore provides an animal
30   selected by using a method according to the invention.
For example, a pig characterised in being homozygous for
an allele in a QTL located at a Sus scrofa chromosome 2
mapping at position 2p1.7 can now be selected and is thus
provided by the invention. Since said QTL is related to
35   the potential muscle mass and/or fat deposition of said
pig and/or said QTL comprises at least a part of a Sus
scrofa insulin-like growth factor-2 (IGF2) allele, it is

possible to select promising pigs to be used for breeding
or to be slaughtered. In particular an animal according
to the invention which is a male is provided. Such a
male, or its sperm or an embryo derived thereof can·
5   advantageously be used in breeding animals for creating
breeding lines or for finally breeding animals destined
for slaughter. In a preferred embodiment of such use as
provided by the invention, a male, or its sperm,
deliberately selected for being homozygous for an allele
10   causing the extreme muscular hyperthrophy and leanness,
is used to produce offspring heterozygous for such an
allele. Due to said allele's paternal expression, said
offspring will also show the favourable traits for
example related to muscle mass, even if the parent female
15   has a different genetic background. Moreover, it is now
possible to positively select the female(s) for having
different traits, for example related to fertility,
without having a negative effect on the muscle mass trait
that is inherited from the allele from the selected male.
20   For example, earlier such males could occasionally be
seen with Piétrain pigs but genetically it was not
understood how to most profitably use these traits in
breeding programmes.

Furthermore, the invention provides a transgenic
25   animal, sperm and an embryo derived thereof, comprising a
synthetic parentally imprinted QTL or functional fragment
thereof as provided by the invention, i.e. it is provided
by the invention to introduce a favourable recombinant
allele; for example introduce the oestrogen receptor
30   locus related to increased litter size of an animal
homozygously in a parentally imprinted region of a
grandparent animal (for example the father of a hybrid
sow if the region was paternally imprinted and the
grandparent was a boar); to introduce a favourable fat-
35   related allele or muscle mass-related recombinant allele
in a paternally imprinted region, and so on. Recombinant
alleles that are interesting or favourable from the
maternal side or often the ones that have opposite
effects to alleles from the paternal side. For example,

in meat animals such as pigs recombinant alleles linked
with meat quality traits such as intra-muscular fat or
muscle mass could be fixed in the dam lines while
recombinant alleles linked with reduced back fat could be
fixed in the sire lines. Other desirable combinations are
for example fertility and/or milk yield in the female
line with growth rates and/or muscle mass in the male
lines.

The invention is further explained in the detailed
description without limiting the invention.

Detailed description.

Example 1: Wild Boar x Large White intercrosses

Methods

Isolation of an *IGF2* BAC clone and fluorescent *in situ*
hybridization (FISH). *IGF2* primers (F:5'-
GGCAAGTTCTTCCGCTAATGA-3' and R:5'-GCACCGCAGAATTACGACAA-
3') for PCR amplification of a part of the last exon and
3'UTR were designed on the basis of a porcine IGF2 cDNA
sequence (GenBank X56094). The primers were used to
screen a porcine BAC library and the clone 253G10 was
isolated. Crude BAC DNA was prepared as described[24]. The
BAC DNA was linearized with *Eco*RV and purified with
QIAEXII (QIAGEN GmbH, Germany). The clone was labeled
with biotin-14-dATP using the GIBCO-BRL Bionick labeling
system (BRL18246-015). Porcine metaphase chromosomes were
obtained from pokeweed (Seromed) stimulated lymphocytes
using standard techniques. The slides were aged for two
days at room temperature and then kept at $-20^{\circ}C$ until
use. FISH analysis was carried out as previously
described[25]. The final concentration of the probe in the
hybridization mix was 10 ng/µl. Repetitive sequences were
suppressed with standard concentrations of porcine

genomic DNA. After post-hybridization washing, the
biotinylated probe was detected with two layers of
avidin-FITC (Vector A-2011). The chromosomes were
counterstained with 0.3 mg/ml DAPI (4,6-Diamino-2-

5   phenylindole; Sigma D9542), which produced a G-banding
like pattern. No posthybridization banding was needed,
since chromosome 2 is easily recognized without banding.
A total of 20 metaphase spreads were examined under an
Olympus BX-60 fluorescence microscope connected to an

10   IMAC-CCD S30 video camera and equipped with an ISIS 1.65
(Metasystems) software.

Sequence, microsatellite, and linkage analysis.

15   About two µg of linearized and purified BAC DNA was used
for direct sequencing with 20 pmoles of primers and
BigDye Terminator chemistry (Perkin Elmer, USA). DNA
sequencing was done from the 3' end of the last exon
towards the 3' end of the UTR until a microsatellite was

20   detected. A primer set (F:5'-GTTTCTCCTGTACCCACACGCATCCC-
3' and R:5'-Fluorescein- CTACAAGCTGGGCTCAGGG-3') was
designed for the amplification of the *IGF2* microsatellite
which is about 250 bp long and located approximately 800
bp downstream from the stop codon. The microsatellite was

25   PCR amplified using fluorescently labeled primers and the
genotyping was carried out using an ABI377 sequencer and
the GeneScan/Genotyper softwares (Perkin Elmer, USA).
Two-point and multipoint linkage analysis were done with
the Cri-Map software[26].

30

Animals and phenotypic data.

The intercross pedigree comprised two European Wild Boar
males and eight Large White females, 4 F_1 males and 22 F_1

35   females, and 200 F_2 progeny[1]. The F_2 animals were
sacrificed at a live weight of at least 80 kg or at a

5   maximum age of 190 days. Phenotypic data on birth weight,
     growth, fat deposition, body composition, weight of
     internal organs, and meat quality were collected; a
     detailed description of the phenotypic traits are

5   provided by Andersson et al.[1] and Andersson-Eklund et
     al.[4]

     Statistical analysis.

10   Interval mapping for the presence of QTL were carried out
     with a least squares method developed for the analysis of
     crosses between outbred lines[27]. The method is based on
     the assumption that the two divergent lines are fixed for
     alternative QTL alleles. There are four possible
15   genotypes in the F_2 generation as regards the
     grandparental origin of the alleles at each locus. This
     makes it possible to fit three effects: additive,
     dominance, and imprinting[2]. The latter is estimated as
     the difference between the two types of heterozygotes,
20   the one receiving the Wild Boar allele through an F_1 sire
     and the one receiving it from an F_1 dam. An F-ratio was
     calculated using this model (with 3 d.f.) versus a
     reduced model without a QTL effect for each cM of
     chromosome 2. The most likely position of a QTL was
25   obtained as the location giving the highest F-ratio.
     Genome-wise significance thresholds were obtained
     empirically by a permutation test[28] as described[2]. The
     QTL model including an imprinting effect was compared
     with a model without imprinting (with 1 d.f.) to test
30   whether the imprinting effect was significant.
         The statistical models also included the fixed
     effects and covariates that were relevant for the
     respective traits; see Andersson-Eklund et al.[4] for a
     more detailed description of the statistical models used.
35   Family was included to account for background genetic

effects and maternal effects. Carcass weight was included
as a covariate to discern QTL effects on correlated
traits, which means that all results concerning body
composition were compared at equal weights. Least-squares

5   means for each genotype class at the *IGF2* locus were
estimated with a single point analysis using Procedure
GLM of SAS[29]; the model included the same fixed effects
and covariates as used in the interval mapping analyses.
The QTL shows a clear parent of origin-specific

10   expression and the map position coincides with that of
the insulin-like growth factor II gene (*IGF2*), indicating
IGF2 as the causative gene. A highly significant
segregation distortion (excess of Wild Boar-derived
alleles) was also observed at this locus. The results

15   demonstrate an important effect of the *IGF2* region on
postnatal development and it is possible that the
presence of a paternally expressed *IGF2*-linked QTL in
humans and in rodent model organisms has so far been
overlooked due to experimental design or statistical

20   treatment of data. The study has also important
implications for quantitative genetics theory and
practical pig breeding.

     IGF2 was identified as a positional candidate gene
for this QTL due to the observed similarity between pig

25   chromosome 2p and human chromosome 11p. A genomic *IGF2*
clone was isolated by screening a porcine BAC library.
FISH analysis with this BAC clone gave a strong
consistent signal on the terminal part of chromosome 2p
(Fig. 1). A polymorphic microsatellite is located in the

30   3'UTR of *IGF2* in mice (GenBank U71085), humans (GenBank
S62623), and horse (GenBank AF020598). The possible
presence of a corresponding porcine microsatellite was
investigated by direct sequencing of the *IGF2* 3'UTR using
the BAC clone. A complex microsatellite was identified

35   about 800 bp downstream of the stop codon; a sequence
comparison revealed that this microsatellite is identical

to a previously described anonymous microsatellite, Swc9[6]. PCR primers were designed and the microsatellite (IGF2ms) was found to be highly polymorphic with three different alleles among the two Wild Boar founders and

5   another two among the eight Large White founders. IGF2ms was fully informative in the intercross as the breed of origin as well as the parent of origin could be determined with confidence for each allele in each F_2 animal.

10   A linkage analysis using the intercross pedigree was carried out with IGF2ms and the microsatellites Sw2443, Sw2623, and Swr2516, all from the distal end of 2p[7]. IGF2 was firmly assigned to 2p by highly significant lod scores (e.g. Z=89.0, θ=0.003 against Swr2516). Multipoint

15   analyses, including previously typed chromosome 2 markers[8], revealed the following order of loci (sex-average map distances in Kosambi cM): Sw2443/Swr2516-0.3-IGF2-14.9-Sw2623-10.3-Sw256. No recombinant was observed between Sw2443 and Swr2516, and the suggested proximal

20   location of IGF2 in relation to these loci is based on a single recombinant giving a lod score support of 0.8 for the reported order. The most distal marker in our previous QTL study, Sw256, is located about 25 cM from the distal end of the linkage group.

25   QTL analyses of body composition, fatness, meat quality, and growth traits were carried out with the new chromosome 2 map using a statistical model testing for the possible presence of an imprinting effect as expected for IGF2. Clear evidence for a paternally expressed QTL

30   located at the very distal tip of 2p was obtained (Fig. 2; Table 1). The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F_2 population. Large effects on the area of the longissumus dorsi muscle, on

35   the weight of the heart, and on back-fat thickness

(subcutaneous fat) were also noted. A moderate effect on
one meat quality trait, reflectance value, was indicated.
The QTL had no significant effect on abdominal fat, birth
weight, growth, weight of liver, kidney, or spleen (data
not shown). The Large White allele at this QTL was
associated with larger muscle mass and reduced back-fat
thickness consistent with the difference between this
breed and the Wild Boar population. The strong imprinting
effect observed for all affected traits strongly suggests
a single causative locus. The pleiotropic effects on
skeletal muscle mass and the size of the heart appear
adaptive from a physiological point of view as a larger
muscle mass requires a larger cardiac output. The clear
paternal expression of this QTL is illustrated by the
least squares means which fall into two classes following
the population origin of the paternally inherited allele
(Table 1). It is worth noticing though that there was a
non-significant trend towards less extreme values for the
two heterozygous classes, in particular for the estimated
effect on the area of longissimus dorsi. This may be due
to chance, but could have a biological explanation, e.g.
that there is some expression of the maternally inherited
allele or that there is a linked, non-imprinted QTL with
minor effects on the traits in question.

        The $IGF2$-linked QTL and the $FAT1$ QTL on chromosome 4
1, 9 are by far the two loci with the largest effect on
body composition and fatness segregating in this Wild
Boar intercross. The $IGF2$ QTL controls primarily muscle
mass whereas $FAT1$ has major effects on fat deposition
including abdominal fat, a trait that was not affected by
the $IGF2$ QTL (Fig. 2). No significant interaction between
the two loci was indicated and they control a very large
proportion of the residual phenotypic variance in the F_2
generation. A model including both QTLs explains 33.1% of
the variance for percentage lean meat in ham, 31.3% for
the percentage of lean meat plus bone in back, and 26.2%

for average back fat depth (compare with a model
including only chromosome 2 effects, Table 1). The two
QTLs must have played a major role in the response during
selection for lean growth and muscle mass in the Large
5   White domestic pig.

A highly significant segregation distortion was
observed in the *IGF2* region (excess of Wild Boar-derived
alleles) as shown in Table 1 ($\chi 2=11.7$, d.f.=2; P=0.003).
The frequency of Wild Boar-derived *IGF2* alleles was 59%
10   in contrast to the expected 50% and there was twice as
many "Wild Boar" as "Large White" homozygotes. This
deviation was observed with all three loci at the distal
tip and is thus not due to typing errors. The effect was
also observed with other loci but the degree of
15   distortion decreased as a function of the distance to the
distal tip of the chromosome. Blood samples for DNA
preparation were collected at 12 weeks of age and we are
convinced that the deviation from expected Mendelian
ratios was present at birth as the number of animals lost
20   prior to blood sampling was not sufficient to cause a
deviation of this magnitude. No other of the more than
250 loci analyzed in this pedigree show such a marked
segregation distortion (L. Andersson, unpublished). The
segregation distortion did not show an imprinting effect,
25   as the frequencies of the two reciprocal types of
heterozygotes were identical (Table 1). This does not
exclude the possibility that the QTL effects and the
segregation distortion are controlled by the same locus.
The segregation distortion maybe due to meiotic drive
30   favoring the paternally expressed allele during
gametogenesis, as the F_1 parents were all sired by Wild
Boar males. Another possibility is that the segregation
distortion may be due to codominant expression of the
maternal and paternal allele in some tissues and/or
35   during a critical period of embryo development. Biallelic
IGF2 expression has been reported to occur to some extent

during human development[10, 11] and interestingly a strong
influence of the parental species background on *IGF2*
expression was recently found in a cross between *Mus*
musculus and *Mus spretus*[12]. It is also interesting that a

5   VNTR polymorphism at the insulin gene, which is very
closely linked to *IGF2*, is associated with size at birth
in humans[13]. It is possible that the *IGF2*-linked QTL in
pigs has a minor effect on birth weight but in our data
it was far from significant (Fig. 2) and there was no

10   indication of an imprinting effect.

     This study is an advance in the general knowledge
concerning the biological importance of the *IGF2* locus.
The important role of *IGF2* for prenatal development is
well-documented from knock-out mice[14] as well as from its

15   causative role in the human Beckwith-Wiedemann
syndrome[15]. This study demonstrates an important role for
the *IGF2*-region also for postnatal development. It should
be stressed that our intercross between outbred
populations is particularly powerful to detect QTL with a

20   parent of origin-specific effect on a multifactorial
trait. This is because multiple alleles (or haplotypes)
are segregating and we could deduce whether a
heterozygous F₂ animal received the Wild Boar allele from
the F₁ male or female. It is quite possible that the

25   segregation of a paternally expressed *IGF2*-linked QTL
affecting a trait like obesity has been overlooked in
human studies or in intercrosses between inbred rodent
populations because of experimental design or statistical
treatment of data. An imprinting effect cannot be

30   detected in an intercross between two inbred lines as
only two alleles are segregating at each locus. Our
result has therefore significant bearings on the future
analysis of the association between genetic polymorphism
in the *insulin-IGF2* region and Type I diabetes[16],

35   obesity[17], and variation in birth weight[13] in humans, as

well as for the genetic dissection of complex traits
using inbred rodent models. A major impetus for
generating an intercross between the domestic pig and its
wild ancestor was to explore the possibilities to map and
5   identify major loci that have responded to selection. We
have now showed that two single QTLs on chromosome 2
(this study) and 4[1, 2] explain as much as one third of
the phenotypic variance for lean meat content in the F_2
generation. This is a gross deviation from the underlying
10   assumption in the classical infinitesimal model in
quantitative genetics theory namely that quantitative
traits are controlled by an infinite number of loci each
with an infinitesimal effect. If a large proportion of
the genetic difference between two divergent populations
15   (e.g. Wild Boar and Large White) is controlled by a few
loci, one would assume that selection would quickly fix
QTL alleles with large effects leading to a selection
plateau. However, this is not the experience in animal
breeding programs or selection experiments where good
20   persistent long-term selection responses are generally
obtained, provided that the effective population size is
reasonably large[18]. A possible explanation for this
paradox is that QTL alleles controlling a large
proportion of genetic differences between two populations
25   may be due to several consecutive mutations; this may be
mutations in the same gene or at several closely linked
genes affecting the same trait. It has been argued that
new mutations contribute substantially to long-term
selection responses[19], but the genomic distribution of
30   such mutations are unknown.

The search for a single causative mutation is the
paradigm as regards the analysis of genetic defects in
mice and monogenic disorders in humans. We propose that
this may not be the case for loci that have been under
35   selection for a large number of generations in domestic
animals, crops, or natural populations. This hypothesis

predicts the presence of multiple alleles at major QTL.
It gains some support from our recent characterization of
porcine coat color variation. We have found that both the
alleles for dominant white color and for black-spotting

5   differ from the corresponding wild-type alleles by at
least two consecutive mutations with phenotypic effects
at the KIT and MC1R loci, respectively[20, 21]. In this
context it is highly interesting that in the accompanying
example we have identified a third allele at the IGF2-

10   linked QTL. The effects on muscle mass of the three
alleles rank in the same order as the breeds in which
they are found i.e. Piétrain pigs are more muscular than
Large White pigs that in turn have higher lean meat
content than Wild Boars.

15   There are good reasons to decide that IGF2 is the
causative gene for the now reported QTL. Firstly, there
is a perfect agreement in map localization (Fig. 2).
Secondly, it has been shown that IGF2 is paternally
expressed in mice, humans, and now in pigs, like the QTL.

20   There are several other imprinted genes in the near
vicinity of IGF2 in mice and humans (Mash2, INS2, H19,
KVLQT1, TAPA1/CD81, and CDKN1C/p57^{KIP2}) but only IGF2 is
paternally expressed in adult tissues[22]. We believe that
this locus provides a unique opportunity for molecular

25   characterization of a QTL. The clear paternal expression
can be used to exclude genes that do not show this mode
of inheritance. Moreover, the presence of an allelic
series should facilitate the difficult distinction
between causative mutations and linked neutral

30   polymorphism. We have already shown that there is no
difference in coding sequence between IGF2 alleles from
Piétrain and Large White pigs suggesting that the
causative mutations occur in regulatory sequences. An
obvious step is to sequence the entire IGF2 gene and its

35   multiple promoters from the three populations. The recent

report that a VNTR polymorphism in the promoter region of
the insulin (INS) gene affects IGF2 expression[23] suggests
that the causative mutations may be at a considerable
distance from the IGF2 coding sequence.

5   The results have several important implications for
the pig breeding industry. They show that genetic
imprinting is not an esoteric academic question but need
to be considered in practical breeding programs. The
detection of three different alleles in Wild Boar, Large
10   White, and Piétrain populations indicates that further
alleles at the IGF2-linked QTL segregate within
commercial populations. The paternal expression of the
QTL facilitates its detection using large paternal half-
sib families as the female contribution can be ignored.
15   The QTL is exploited to improve lean meat content by
marker assisted selection within populations or by marker
assisted introgression of favorable alleles from one
population to another.

Example 2: Piétrain x Large White intercrosses

Methods

Pedigree material: The pedigree material utilized to map
QTL was selected from a previously described Piétrain x
Large White F2 pedigree comprising > 1,800 individuals[6,7].
To assemble this F2 material, 27 Piétrain boars were
mated to 20 Large White sows to generate an F1 generation
comprising 456 individuals. 31 F1 boars were mated to
unrelated 82 F1 sows from 1984 to 1989, yielding a total
of 1862 F2 offspring. F1 boars were mated on average to 7
females, and F1 sows to an average of 2,7 males. Average
offspring per boar were 60 and per sow 23.

Phenotypic information: (i) *Data collection:* A total of
21 distinct phenotypes were recorded in the F2
generation[6,7]. These included:
- five growth traits: birth weight (g), weaning weight
(Kg), grower weight (Kg), finisher weight (Kg) and
average daily gain (ADG; Kg/day; grower to finsher
period);
- two body proportion measurements: carcass length (cm);
and a conformation score (0 to 10 scale; ref.6);
- ten measurements of carcass composition obtained by
dissection of the chilled carcasses 24 hours after
slaughter. These include measurements of muscularity: %
ham (weight hams/carcass weight), % loin (weight
loin/carcass weight), % shoulder (weight
shoulder/carcass weight), % lean cuts (% ham + %loin + %
shoulder); and measurements of fatness: average back-fat
thickness (BFT; cm), % backfat (weight backfat/carcass
weight), % belly (weight belly/carcass weight), % leaf
fat (weight leaf fat/carcass weight), % jowl (weight
jowl/carcass weight), and "% fat cuts" (% backfat + %
belly + % leaft fat + % jowl).
- four meat quality measurements: pH $_{LD1}$ (*Longissimus dorsi* 1

hour after slaughter), pH $_{LD24}$ (*Longissimus dorsi* 24 hours
after slaughter), pH $_{G1}$ (*Gracilis* 1 hour after slaughter) and
pH $_{G24}$ (*Gracilis* 24 hours after slaughter). *(ii) Data*
processing: Individual phenotypes were preadjusted for fixed

5   effects (sire, dam, CRC genotype, sex, year-season, parity)
and covariates (litter size, birth weight, weaning weight,
grower weight, finisher weight) that proved to significantly
affect the corresponding trait. Variables included in the
model were selected by stepwise regression.

10

Marker genotyping: Primer pairs utilized for PCR
amplification of microsatellite markers are as described[19].
Marker genotyping was performed as previously described[20].
Genotypes at the *CRC* and *MyoD* loci were determined using

15   conventional methods as described[1,12]. The LAR test for the
Igf2 SNP was developed according to Baron et al.[21] using a
primer pair for PCR amplification (5'-
CCCCTGAACTTGAGGACGAGCAGCC-3';5'-ATCGCTGTGGGCTGGGTGGGCTGCC-3'
) and a set of three primers for the LAR step (5'-FAM-

20   CGCCCCAGCTGCCCCCCAG-3'; 5'-HEX-CGCCCCAGCTGCCCCCCAA-3'; 5'-
CCTGAGCTGCAGCAGGCCAG-3').

Map construction: Marker maps were constructed using the
TWOPOINT, BUILD and CHROMPIC options of the CRIMAP package[22].

25   To allow utilisation of this package, full-sib families
related via the boar or sow were disconnected and treated
independently. By doing so, some potentially usable
information was neglected, yielding, however, unbiased
estimates of recombination rates.

30

QTL mapping: (i) Mapping Mendelian QTL: Conventional QTL
mapping was performed using a multipoint maximum likelihood
method.   The applied model assumed one segregating QTL per

chromosome, and fixation of alternate QTL alleles in the
respective parental lines, Piétrain (P) and Large White (LW).
A specific analysis program had to be developed to account
for the missing genotypes of the parental generation,

5   resulting in the fact that the parental origin of the F1
chromosomes could not be determined. Using a typical
"interval mapping" strategy, an hypothetical QTL was moved
along the marker map using user-defined steps. At each
position, the likelihood (L) of the pedigree data was

10   computed as:

$$L = \sum_{\varphi=1}^{2^r} \prod_{i=1}^{n} \sum_{G=1}^{4} (P(G|M_i,\theta,\varphi)P(y_i|G))$$

P or right chromosme P), there is a total of 2^r combinations
for r F1 parents.

15   $\prod_{i=1}^{n}$ n F2

$\sum_{G=1}^{4}$ ith F2 offspring, over the four possible QTL genotypes:

P/P, P/LW, LW/P and LW/LW

$P(G|M_i,\theta,\varphi)M_i$: the marker genotype of the ith F2 offspring and
its F1 parents, (ii) : the vector of recombination rates

20   between adjacent markers and between the hypothetical QTL and
its flanking markers, and (iii) θ the considered marker-QTL
phase combination of the F1 parents.
Recombination rates and marker linkage phase of F1 parents
are assumed to be known when computing this probability. Both

25   were determined using CRIMAP in the map construction phase
(see above).

$P(y_i|G) y_i$) of offspring i, given the QTL genotype under
consideration. This probability is computed from the normal
density function:

$$P(y_i|G) = \frac{1}{\sqrt{2\pi}\sigma} e^{\frac{-(y_i - \mu_G)^n}{2\sigma^2}}$$

$_G$ is the phenotypic mean of the considered QTL genotype (PP, PL, LP or LL) and σ^2 the residual variance σ^2 was considered to be the same for the four QTL genotypic classes.

5   The values of μ_{PP}, $\mu_{PL} = \mu_{LP}$, μ_{LL} and σ^2 maximizing L were determined using the GEMINI optimisation routine[23].

The likelihood obtained under this alternative H_1 hypothesis was compared with the likelihood obtained under the null hypothesis H_0 of no QTL, in which the phenotypic means of the

10   four QTL genotypic classes were forced to be identical. The difference between the logarithms of the corresponding likelihoods yields a lodscore measuring the evidence in favour of a QTL at the corresponding map position.

*(ii) Significance thresholds:*Following Lander & Botstein[24],

15   lodscore thresholds *(T)* associated with a chosen genome-wise significance level, were computed such that:

$$\alpha = (C + 9.21 GT) \chi_i^2 (4.6T)$$

C corresponds to the number of chromosomes (= 19), G corresponds to the length of the genome in Morgans (= 29),

20   and χ_2^1 *(4.6T)* denotes one minus the cumulative distribution function of the chi-squared distribution with 2 d.f. Single point $2\ln(LR)$ were assumed to be distributed as a chi-squared distribution with two degrees of freedom, as we were fitting both an additive and dominance component. To account for the

25   fact that we were analysing multiple traits, significance levels were adjusted by applying a Bonferoni correction corresponding to the effective number of independent traits that were analyzed. This effective number was estimated at 16 following the approach described by Spelman et al.[25].

30   Altogether, this allowed us to set the lodscore threshold associated with an experiment-wise significance level of 5%

at 5.8. When attempting to confirm the identified QTL in an
independent sample, the same approach was used, however,
setting C at 1, G at 25cM and correcting for the analysis of
4.5 independent traits (as only six traits were analyzed in
5   this sample). This yielded a lodscore threshold associated
with a Type I error of 5% of 2.

(iii). *Testing for an imprinted QTL:* To test for an imprinted
QTL, we assumed that only the QTL alleles transmitted by the
parent of a given sex would have an effect on phenotype, the
10   QTL alleles transmitted by the other parent being "neutral".
The likelihood of the pedigree data under this hypothesis was
computed using equation 1. To compute $P(y_i \mid G)$, however, the
phenotypic means of the four QTL genotypes were set at $\mu_{PP} =
\mu_{PL} = \mu_P$ and $\mu_{LP} = \mu_{LL} = \mu_L$ to test for a QTL for which the
15   paternal allele only is expressed, and $\mu_{PP} = \mu_{LP} = \mu_P$ and $\mu_{PL} =
\mu_{LL} = \mu_L$ to test for a QTL for which the maternal allele only
is expressed. It is assumed in this notation that the first
subscript refers to the paternal allele, the second subscript
to the maternal allele. H_0 was defined as the null-hypothesis
20   of no QTL, H_1 testing the presence of a Mendelian QTL; H_2
testing the presence of a paternally expressed QTL, and H_3
testing the presence of a maternally expressed QTL.

RT-PCR: Total RNA was extracted from skeletal muscle
25   according to Chirgwin et al.[26]. RT-PCR was performed using
the Gene-Amp RNA PCR Kit (Perkin-Elmer) The PCR products were
purified using QiaQuick PCR Purification kit (Qiagen) and
sequenced using Dye terminator Cycle Sequencing Ready
Reaction (Perkin Elmer) and an ABI373 automatic sequencer.

In example 2 we report the identification of a QTL with major
effect on muscle mass and fat deposition mapping to porcine
2p1.7 The QTL shows clear evidence for parental imprinting
strongly suggesting the involvement of the *Igf2* locus.

5   A Piétrain X Large White intercross comprising 1125 F_2
offspring was generated as described[6,7]. The Large White and
Piétrain parental breeds differ for a number of economically
important phenotypes. Piétrains are famed for their
exceptional muscularity and leannes [8] (Figure 2), while Large

10   Whites show superior growth performance. Twenty-one distinct
phenotypes measuring (i) growth performance (5), (ii)
muscularity (6), (iii) fat deposition (6), and (iv) meat
quality (4), were recorded on all F_2 offspring.

In order to map QTL underlying the genetic differences

15   between these breeds, we undertook a whole genome scan using
microsatellite markers on an initial sample of 677 F_2
individuals. Analysis of pig chromosome 2 using a ML
multipoint algorithm, revealed highly significant lodscores
(up to 20) for six of the 12 phenotypes measuring muscularity

20   and fat deposition at the distal end of the short arm of
chromosome 2 (Figure 3a). Positive lodscores were obtained
for the remaining six phenotypes, however, not reaching the
genome-wise significance threshold (= 5%). To confirm this
finding, the remaining sample of 355 F_2 offspring was

25   genotyped for the five most distal 2p markers and QTL
analysis performed for the traits yielding the highest
lodscores in the first analysis. Lodscores ranged from 2.1 to
7.7, clearly confirming the presence of a major QTL in this
region. Table 2 reports the corresponding ML estimates for

30   the three genotypic means as well as the corresponding
residual variance.

Bidirectional chromosome painting establishes a
correspondence between SSC2p and HSA11pter-q13[9,10]. At least

two serious candidate genes map to this region in man: the
myogenic basic helix-loop-helix factor, *MyoD*, maps to
HSA11p15.4, while *Igf2* maps to HSA11p15.5 *MyoD* is a well
known key regulator of myogenesis and is one of the first
5   myogenic markers to be switched on during development[11]. A
previously described amplified sequence polymorphism in the
porcine *MyoD* gene[12] proved to segregate in our F_2 material,
which was entirely genotyped for this marker. Linkage
analysis positioned the *MyoD* gene in the SW240-SW776 (odds >
10   1000) interval, therefore well outside the lod-2 drop off
support interval for the QTL (figure 1). *Igf2* is known to
enhance both proliferation and differentiation of myoblasts
in vitro[13] and to cause a muscular hypertrophy when
overexpressed *in vivo*. Based on a published porcine adult
15   liver cDNA sequence[14], we designed primer pairs allowing us
to amplify the entire *Igf2* coding sequence with 222 bp of
leader and 280 bp of trailor sequence from adult skeletal
muscle cDNA. Piétrain and Large White RT-PCR products were
sequenced indicating that the coding sequences was identical
20   in both breeds and with the published sequence. However, a G
A transition was found in the leader sequence corresponding
to exon 2 in man (Figure 4). We developed a screening test
for this single nucleotide polymorphism (SNP) based on the
ligation amplification reaction (LAR), allowing us to
25   genotype our pedigree material. Based on these data, *Igf2* was
shown to colocalize with the SWC9 microsatellite marker (=
0%), therefore located at approximately 2 centimorgan from
the most likely position of the QTL and well within the 95%
support interval for the QTL (figure 1). Subsequent sequence
30   analysis demonstrated that the microsatellite marker SWC9 is
actually located within the 3' UTR of the *Igf2* gene. Combined
with available comparative mapping data for the PGA and FSH
loci, these results suggest the occurrence of an interstitial

inversion of a chromosome segment containing *MyoD*, but not
Igf2 which has remained telomeric in both species.

Igf2 therefore appeared as a strong positional allele
having the observed QTL effect. In man and mouse, *Igf2* is
5 known to be imprinted and to be expressed exclusively from
the paternal allele in several tissues[15]. Analysis of
skeletal muscle cDNA from pigs heterozygous for the SNP
and/or SWC9, shows that the same imprinting holds in this
tissue in the pig as well (Figure 4). Therefore if *Igf2* were
10 responsible for the observed effect, and knowing that only
the paternal *Igf2* allele is expressed, one can predict that
(i) the paternal allele transmitted by F1 boars (P or LW)
would have an effect on phenotype of F2 offspring, (ii) the
maternal allele transmitted by F1 sows (P or LW) would have
15 no effect on phenotype of F2 offspring, and (iii) the
likelihood of the data would be superior under a model of a
bimodal (1:1) F2 population sorted by inherited paternal
allele when compared to a conventional "Mendelian" model of a
trimodal (1:2:1) F2 population. The QTL mapping programs were
20 adapted in order to allow testing of the corresponding
hypotheses. H_0 was defined as the null-hypothesis of no QTL,
H_1 as testing for the presence of a Mendelian QTL, H_2 as
testing for the presence of a paternally expressed QTL, and
H_3 as testing for the presence of a maternally expressed QTL.
25 Figure 3 summarizes the obtained results. Figure 3a, 3b
and 3c respectively show the lodscore curves corresponding to
$\log_{10} (H_2/H_0)$, $\log_{10} (H_3/H_0)$ and $\log_{10} (H_2/H_1)$. It can be seen
that very significant lodscores are obtained when testing for
the presence of a paternally expressed QTL, while there is no
30 evidence at all for the segregation of a QTL when studying
the chromosomes transmitted by the sows. Also, the hypothesis
of a paternally expressed QTL is significantly more likely (
$\log_{10} (H_2/H_1) > 3$) than the hypothesis of a "Mendelian" QTL

for all examined traits. The fact that the same tendency is
observed for all traits indicates that it is likely the same
imprinted gene that is responsible for the effects observed
on the different traits. Table 2 reports the ML phenotypic
means for the F2 offspring sorted by inherited paternal QTL
allele. Note that when performing the analysis under a model
of a mendelian QTL, the Piétrain and Large White QTL alleles
appeared to behave in an additive fashion, the heterozygous
genotype exhibiting a phenotypic mean corresponding exactly
to the midpoint between the two homzygous genotypes. This is
exactly what one would predict when dealing with an imprinted
QTL as halve of the heterozygous offspring are expected to
have inherited the P allele from their sire, the other halve
the LW allele.

These data therefore confirmed our hypothesis of the
involvement of an imprinted gene expressed exclusively from
the paternal allele. The fact that the identified chromosomal
segment coincides precisely with an imprinted domain
documented in man and mice strongly implicates the
orthologous region in pigs. At least seven imprinted genes
mapping to this domain have been documented (*Igf2*, *Ins2*, *H19*,
Mash2, *p57^{KIP2}*, *K_vLQTL1* and *TDAG51*) (ref. 15 and Andrew
Feinberg, personal communication). Amongst these, only *Igf2*
and *Ins2* are paternally expressed. While we cannot exclude
that the observed QTL effect is due to an as of yet
unidentified imprinted gene in this region, its reported
effects on myogenesis *in vitro* and *in vivo*[3] strongly
implicate *Igf2*. Particularly the muscular hypertrophy
observed in transgenic mice overexpressing *Igf2* from a muscle
specific promotor are in support of this hypothesis (Nadia
Rosenthal, personal communication. Note that allelic variants
of the *INS* VNTR have recently been shown to be associated

with size at birth' in man[16], and that the same VNTR has been
shown to affect the level of *Igf2* expression[17].

5   The observation of the same QTL effect in a Large White
x Wild Boar intercross indicates the existence of a series of
at least three distinct functional alleles. Moreover,
preliminary evidence based on marker assisted segregation
analysis points towards residual segregation at this locus
within the Piétrain population (data not shown). The
occurrence of an allelic series might be invaluable in
10   identifying the causal polymorphisms which - based on the
quantitatve nature of the observed effect - are unlikely to
be gross gene alterations but rather subtle regulatory
mutations.

       The effects of the identified QTL on muscle mass and fat
15   deposition are truly major, being of the same magnitude of
those reported for the *CRC* locus[6,7] though apparently without
the associated deleterious effects on meat quality. We
estimate that both loci jointly explain close to 50% of the
Piétrain versus Large White breed difference for muscularity
20   and leanness. Understanding the parent-of-origin effect
characterizing this locus will allow for its optimal use in
breeding programs. Indeed, today half of the offspring from
commercially popular Piétrain x Large White crossbred boars
inherit the unfavourable Large White allele causing
25   considerable loss.

       The QTL described in this work is the second example of
a gene affecting muscle development in livestock species that
exhibits a non-mendelian inheritance pattern. Indeed, we have
previously shown that the callipyge locus (related to the
30   qualitative trait wherein muscles are doubled) is
characterized by polar overdominance in which only the
heterozygous individuals that inherit the CLPG mutation from
their sire express the double-muscling phenotype[5]. This

42

demonstrates that 'parent-of-origin effects affecting genes
underlying production traits in livestock might be relatively
common.

5   Example 3:

Generating a reference sequence of IGF2 and flanking loci in
the pig.

10   The invention provides an imprinted QTL with major effect on
muscle mass mapping to the IGF2 locus in the pig, and use of
the QTL as tool in marker assisted selection. To fine tune
this tool for marker assisted selection, as well as to
further identify a causal mutation, we have further generated
15   a reference sequence encompassing the entire porcine IGF2
sequence as well as that from flanking genes.

To achieve this, we screened a porcine BAC library with IGF2
probes and identified two BACs. BAC-PIGF2-1 proved to
20   contain the INS and IGF2 genes, while BAC-PIGF2-2 proved to
contain the IGF2 and H19 genes. The NotI map as well as the
relative position of the two BACs is shown in Figure 5. BAC-
PIGF2-1 was shotgun sequenced using standard procedures and
automatic sequencers. The resulting sequences were assembled
25   using standard software yielding a total of 115 contigs. The
corresponding sequences are reported in figure 6. Similarity
searches were performed between the porcine contigs and the
orthologous sequences in human. Significant homologies were
detected for 18 contigs and are reported in Figure 7.
30
For BAC-PIGF2-2, the 24 Kb NotI fragment not present in BAC-
PIGF2-1 was subcloned and sequenced using the EZ::TN
transposon approach and ABI automatic sequencers. Resulting

sequences were assembled using the Phred-Phrap-Consed program
suit, yielding seven distinct contigs (figure 8). The contig
sequences were aligned with the corresponding orthologous
human sequences using the compare and dotplot programs of the
5 GCG suite. Figure 9 symmarizes the corresponding results.

Example 4: Identification of DNA sequence polymorphisms in
the IGF2 and flanking loci.

10 Based on the reference sequence obtained as described in
Example 1, we resequenced part of the IGF2 and flanking loci
from genomic DNA isolated from Piétrain, Large White and Wild
Boar individuals, allowing identification of DNA sequence
polymorphisms such as reported in figure 10.
15

44

Legends to the figures

Fig. 1: Test statistic curves obtained in QTL analyses of
chromosome 2 in a Wild Boar/Large White intercross. The graph
plots the F ratio testing the hypothesis of a single QTL at a
given position along the chromosome for the traits indicated.
The marker map with the distances between markers in Kosambi
centiMorgan is given on the X-axis. The horizontal lines
represent genome-wise significant (P<0.05) and suggestive
levels for the trait lean meat in ham; similar significance
thresholds were obtained for the other traits.

Figure 2: Piétrain pig with characteristic muscular
hypertrophy.

Figure 3: Lodscore curves obtained in a Piétrain x Large
White intercross for six phenotypes measuring muscle mass and
fat deposition on pig chromosome 2. The most likely positions
of the Igf2 and MyoD genes determined by linkage analysis
with respect to the microsatellite marker map are shown. H_0
was defined as the null-hypothesis of no QTL, H_1 as testing
for the presence of a Mendelian QTL, H_2 as testing for the
presence of a paternally expressed QTL, and H_3 as testing for
the presence of a maternally expressed QTL. 3a: $\log_{10}(H_1/H_0)$,
3b: $\log_{10}(H_2/H_0)$, 3c: $\log_{10}(H_3/H_0)$

Figure 4: A. Structure of the human Igf2 gene according to
ref. 17, with aligned porcine adult liver cDNA sequence as
reported in ref. 16. The position of the nt241(G-A)
transition and Swc9 microsatellite are shown. B. The
corresponding markers were used to demonstrate the
monoallelic (paternal) expression of Igf2 in skeletal muscle

and liver of 10-week old fetuses. PCR amplification of the
nt421 (G-A) polymorphism and Swc9 microsatellite from genomic
DNA clearly shows the heterozygosity of the fetus, while only
the paternal allele is detected in liver cDNA (nt421 (G-A) and

5   Swc9) and muscle cDNA (Swc9). The absence of RT-PCR product
for nt421 (G-A) from in fetal muscle points towards the
absence of mRNA including exon 2 in this tissue. Parental
origin of the foetal alleles was determined from the
genotypes of sire and dam (data not shown).

10
Figure 5: A NotI restriction map showing the relative
position of BAC-PIGF2-1 (comprising INS and IGF2 genes), and
BAC-PIGF2-2 (comprising IGF2 and H19 genes).

15 Figure 6: Nucleic acid sequences of contig 1 to contig 115
derived from BAC-PIGF2-1 which was shotgun sequenced using
standard procedures and automatic sequencers.

Figure 7: Similarity between porcine contigs of figure 6 and
20 orthologous sequences in human.

Figure 8 Nucleic acid sequences of contig 1 to contig 7
derived from BAC-PIGF2-2, (the 24 Kb NotI fragment not
present in BAC-PIGF2-1) which was subcloned and sequenced
25 using the EZ::TN transposon approach and ABI automatic
sequencers.

Figure 9: Similarity between porcine contigs of figure 8 and
orthologous sequences in human.

30
Figure 10: DNA sequence polymorphisms in the IGF2 and
flanking loci from genomic DNA isolated from Piétrain, Large
White and Wild Boar individuals.

REFERENCES

Literature cited with example 1

1.   Andersson, L. et al. Genetic mapping of quantitative

5   trait loci for growth and fatness in pigs. *Science* 263, 1771-1774 (1994).

2.   Knott, S.A. et al. Multiple marker mapping of quantitative trait loci in a cross between outbred wild boar and Large White pigs. *Genetics* 149, 1069-1080 (1998).

10   3.   Edfors-Lilja, I. et al. Mapping quantitative trait loci for immune capacity in the pig. *Journal of Immunology* 161, 829-835 (1998).

4.   Andersson-Eklund, L. et al. Mapping quantitative trait loci for carcass and meat quality traits in a wild boar x

15   Large White intercross. *Journal of Animal Science* 76, 694-700 (1998).

5.   Fronicke, L., Chowdhary, B.P., Scherthan, H. & Gustavsson, I. A comparative map of the porcine and human genomes demonstrates ZOO-FISH and gene mapping-based

20   chromosomal homologies. *Mamm Genome* 7, 285-90 (1996).

6.   Alexander, L.J. et al. Physical assignments of 68 porcine cosmids and lambda clones containing microsatellites. *Mammalian Genome* 7, 368-372 (1996).

7.   Rohrer, G.A. et al. A comprehensive map of the porcine

25   genome. *Genome Research* 6, 371-391 (1996).

8.   Marklund, L. et al. A comprehensive linkage map of the pig based on a wild pig-Large White intercross. *Anim Genet* 27, 255-69 (1996).

9.   Marklund, L., Nyström, P.E., Stern, S., Anderssson-

30   Eklund, L. & Andersson, L. Quantitative trait loci for

fatness and growth on pig chromosome 4. *Heredity* In press(1998).

10. Ohlsson, R., Hedborg, F., Holmgren, L., Walsh, C. & Ekstrom, T.J. Overlapping patterns of IGF2 and H19 expression during human development: biallelic IGF2 expression correlates with a lack of H19 expression. *Development* 120, 361-368 (1994).

11. Ekström, T.J., Cui, H., Li, X. & Ohlsson, R. Promoter-specific IGF2 imprinting status and its plasticity during human liver development. *Development* 121, 309-316 (1995).

12. Hemberger, M. *et al.* H19 and Igf2 are expressed and differentially imprinted in neuroectoderm-derived cells in the mouse brain. *Dev. Genes Evol.* 208, 393-402 (1998).

13. Dunger, D.B. *et al.* Association of the INS VNTR with size at birth. *Nature Genetics* 19, 98-100 (1998).

14. DeChiara, T.M., Robertson, E.J. & Efstratiadis, A. Parental imprinting of the mouse insulin-like growth factor II gene. *Cell* 64, 849-859 (1991).

15. Sun, F.L., Dean, W.L., Kelsey, G., Allen, N.D. & Reik, W. Transactivation of Igf2 in a mouse model of Beckwith-Wiedemann syndrome. *Nature* 389, 809-815 (1997).

16. Davies, J.L. *et al.* A genome-wide search for human type 1 diabetes susceptibility genes. *Nature* 371, 130-136 (1994).

17. O'Dell, S.D. *et al.* ApaI polymorphism in insulin-like growth factor II (IGF2) gene and weight in middle-aged males. *International Journal of Obesity* 21, 822-825 (1997).

18. Falconer, D.S. & Mackay, T.F.C. *Introduction to Quantitative Genetics*, (Longman, England, 1996).

19. Hill, W.G. Rates of change in quantitative traits from fixation of new mutations. *Proc Natl Acad Sci U S A* 79, 142-145 (1982).

20.   Marklund, S. *et al*. Molecular basis for the dominant
white phenotype in the domestic pig. *Genome Research* 8, 826-
. 833 (1998).

21.   Kijas, J.M.H. *et al*. Melanocortin receptor 1 (*MC1R*)
mutations and coat color in the pig. *Genetics* In press(1998).

22.   Beechey, C.V. personal communication (1998).

23.   Paquette, J., Giannoukakis, N., Polychronakos, C.,
Vafiadis, P. & Deal, C. The *INS* 5' variable number of tandem
repeats is associated with *IGF2* expression in humans. *Journal
of Biological Chemistry* 273, 14158-14164 (1998).

24.   Sambrook, J., Fritsch, E.F. &.Maniatis, T. *Molecular
cloning : A laboratory manual*., (Cold Spring Harbor
Laboratory Press, Cold Spring Harbor, 1989).

25.   Chowdhary, B.P., de la Sena, C., Harbitz, I., Eriksson,
L. & Gustavsson, I. FISH on metaphase and interphase
chromosomes demonstrates the physical order of the genes for
GPI, CRC, and LIPE in pigs. *Cytogenetics Cell Genetics* 71,
175-178 (1995).

26.   Green, P., Falls, K. & Crook, S. *Documentation for CRI-
MAP, version 2.4*., (Washington University School of Medicine,
St Louise, MO, 1990).

27.   Haley, C.S., Knott, S.A. & Elsen, J.M. Mapping
quantitative trait loci in crosses between outbred lines
using least squares. *Genetics* 136, 1195-1207 (1994).

28.   Churchill, G.A. & Doerge, R.W. Empirical threshold
values for quantitative trait mapping. *Genetics* 138, 963-971
(1994).

29.   Anonymous. *SAS version 6.10*, (SAS Institute Inc., Cary,
NC., 1990).

References used with example 2:

1. Fuji, J.; Otsu, K.; Zorzato, F.; Deleon, S.; Khanna, V.K.;
Weiler, J.E. O'Brien, P.J.; MacLennan, D.H. (1991).
Identification of a mutation in the porcine ryanodine
receptor associated with malignant hyperthermia. *Science* 253:
5   448-451.

2. MacLennan, D.H. & Phillips, M.S. (1993). Malignant
hyperthermia. *Science* 256:789-794.

3. Grobet, L.; Royo Martin, L.J.; Poncelet, D.; Pirottin, D.;
Brouwers, B.; Riquet, J.; Schoeberlein, A.; Dunner, S.;
10   Ménissier, F.; Massabanda, J.; Fries, R.; Hanset, R.;
Georges, M. (1997) A deletion in the myostatin gene causes
double-muscling in cattle. *Nature Genetics* 17:71-74.

4. Andersson, L.; Haley, C.S.; Ellegren, H.; Knott, S.A.;
Johansson, M.; Andersson, K.; Andersson-Eklund, L.; Edfors-
15   Lilja, I.; Fredholm, M.; Hansson, I.; Håkansson, J.;
Lundström, K. (1994). Genetic mapping of quantitative trait
loci for growth and fatness in pigs. Science 263:1771-1774.

5. Cockett, N.; Jackson, S.; Shaw, T.; Farnir, F.; Berghmans,
S.;Snowder, G.; Nielsen, D.; Georges, M. (1996). Polar
20   overdominance at the ovine callipyge locus. *Science* 273:236-
238

6. Hanset, R.; Dasnois, C.; Scalais, S.; Michaux, C.; Grobet,
L. (1995). Genotypes at the locus for halothane sensitivity
and performance in a Piétrain x Large White F2. Genet. Sel.
25   Evol. 27: 63-76.

7. Hanset, R.; Dasnois, C.; Scalais, S.; Michaux, C.; Grobet,
L. (1995). Introgression into the Piétrain genome of the
normal allele at the locus for halothane sensitivity. Genet.
Sel. Evol. 27: 77-88.

30   8. Olivier, L.; Lauvergne, J.J. (1967). A study of the
inheritance of the muscular hypertrophy of the Piétrain pig:
preliminary results. Annales de Médecine Vétérinaire 111:
104-109.

50

9. Rettenberger, G.; Klett, C.; Zechner, U.; Kunz, J.; Vogel, W.; Hameister, H. (1995). Visualisation of the conservation of synteny between humans and pigs by heterologous chromosome painting. *Genomics* 26: 372-378.

10. Goureau, A.; Yerle, M.; Schmitz, A.; Riquet, J.; Milan, D.; Pinton, P.; Frelat, G.; Gellin, J. (1996). Human and porcine correspondence of chromosome segments using bidirectional chromosome painting. *Genomics* 36:252-262.

11. Yun, K.; Wold, B. (1996). Skeletal muscle determination and differentiation: story of a core regulatory network and its context. Current Opinion in Cell Biology 8:877-889.

12. Knoll, A.; Nebola, M.; Dvorak, J.; Cepica, S. (1997). Detection of a DdeI PCR RFLP within intron 1 of the porcine MYOD1(MYF3) locus. *Animal Genetics* 28, 308-322.

13. Florini, J.R.; Ewton, D.Z.; McWade, F.J. (1995). IGFs, muscle growth, and myogenesis. Diabetes Review 3:73-92.

14. Catchpole, I.R.; Engström, W. (1990). Nucleotide sequence of a porcine insulin-like growth factor II cDNA. Nucleic Acids Research 18(21):6430.

15. Feil, R.; Moore, T.F.; Oswald, J.; Walter, J.; Sun, F.; Reik, W. (1997). The imprinted insulin like growth factor 2 gene. Pp70 In Genomic Imprinting. Eds. Reik & Surani. IRL Press at Oxford University Press.

16. Dunger, D.B.; Ong, K.K.L.; Huxtable, S.J.; Sherriff, A.; Woods, K.A.; Ahmed, M.L.; Golding, J.; Pembrey, M.E.; Ring, S.; the ALSPAC study team, Bennett, S.T.; Todd, J.A. (1998). Association of the INS VNTR with size at birth. *Nature Genetics* 19: 98-100.

17. Paquette J, Giannoukakis N, Polychronakos C, Vafiadis P, Deal C. (1998) The INS 5' variable number of tandem repeats is associated with IGF2 expression in humans. J. Biol Chem 273(23):14158-14164

18. Andersson-Eklund, L.; Marklund, L.; Lundström, K.; Haley,
C.S.; Andersson, K.; Hansson, I.; Moller, M.; Andersson, L.
(1998). Mapping Quantitative Trait Loci for carcass and meat
quality traits in a Wild Boar x Large White intercross. *J.*
5   *Anim. Sci.* 76:694-700.

19. Rohrer, G.A.; Alexander, L.J.; Hu, Z.; Keele, J.W.;
Smith, T.P.; Beattie, C.W. (1996). A comprehensive map of the
porcine genome. Genome Research, in the press.

20. Georges, M.; Nielsen, D.; Mackinnon, M.; Mishra, A.;
10 Okimoto, R.; Pasquino, A.T.; Sargeant, L.S.; Sorensen, A.;
Steele, M.R.; Zhao, X.; Womack, J.E.; Hoeschele, I. (1995).
Mapping quantitative trait loci controlling milk production
by exploiting progeny testing. *Genetics* 139: 907-920.

21. Baron, H.; Fung, S.; Aydin, A.; Bahring, S.; Luft, F.C.;
15 Schuster, H. (1996). Oligonucleotide ligation assay (OLA) for
the diagnosis of familial hypercholesterolemia. Nat.
Biotechnol. 14(10):1279-1282.

22. Lander, E.; Green, P. (1987) Construction of multilocus
genetic linkage maps in humans. Proceedings of National
20 Academy of Science (USA) 84: 2363-2367.

23. Lalouel, J.M. (1983). Optimization of functions. Contrib.
Epidemiol.Biostat. 4:235-259.

24. Lander, E.S. & Botstein, D. (1989). Mapping mendelian
factots underlying quantitative traits using RFLP linkage
25 maps. *Genetics* 121:185-199.

25. Spelman RL, Coppieters W, Karim L, van Arendonk JAM,
Bovenhuis H (1996) Quantitative trait loci analysis for five
milk production traits on chromosome six in the dutch
Holstein-Friesian population. Genetics 144:1799-1808.

30 26.Chirgwin, J.M.; Przybyla, A.E.; MacDonald, R.J.; Rutter, W.J.
(1979) Isolation of biologically active ribonucleic acid from
sources enriched in ribonuclease. *Biochemistry* 18:5294-5299

Table 1 Summary of QTL analysis for pig chromosome 2 in a Wild Boar/Large White intercross[1]

Trait	F ratio[2] QTL	Imprinting	Map position[3]	Percent of F_2 variance[4]	Least squares means[5] wP/wM	wP/LM	LP/wM	LP/LM
					n=62	n=43	n=43	n=30
Body composition traits								
Lean meat in ham, %	24.4***	19.1***	0	30.6	63.6[a]	64.2[a]	66.4[b]	67.3[b]
Lean meat mass in ham, kg	18.1***	16.8****	1	24.3	4.69[a]	4.72[a]	4.94[b]	5.02[b]
Lean meat + bone in back, %	12.2**	9.6**	0	17.4	66.3[a]	66.7[a]	69.3[b]	70.8[b]
Longissimus muscle area, cm²	10.3**	4.8*	1	15.4	31.9[a]	33.0[a]	34.5[b]	35.2[b]
Fatness traits								
Average back fat depth, mm	7.1*	8.7**	0	10.4	27.2[a]	27.7[a]	25.5[b]	24.7[b]
Weight of internal organs								
Heart, gram	9.7**	11.4***	0	14.4	226[a]	225[a]	238[b]	244[b]
Meat quality traits								
Reflectance value, EEL	5.7	6.1*	1	8.1	18.6[a]	18.4[a]	21.8[b]	19.7[a]

*P<0.05; **P<0.01; ***P<0.001

SUBSTITUTE SHEET (RULE 26)

Table 1, continued

[1]Only the traits for which the QTL peak was in the *IGF2*

5 region (0-10 cM) and the test statistic reached the nominal

significance threshold of F=3.9 are included.

[2]"*QTL*" is the test statistic for the presence of a QTL under

a genetic model with additive, dominance, and imprinting

effects (3 d.f.) while "Imprinting" is the test statistic for

10 the presence of an imprinting effect (1 d.f.), both obtained

at the position of the QTL peak. Genome-wise significance

thresholds, estimated by permutation, were used for the QTL

test while nominal significance thresholds were used for the

Imprinting test.

15 [3]In cM from the distal end of 2p; *IGF2* is located at 0.3 cM.

[4]The reduction in the residual variance of the F_2 population

effected by inclusion of an imprinted QTL at the given

position.

[5]Means and standard errors estimated at the *IGF2* locus by

20 classifying the genotypes according to the population and

parent of origin of each allele. *W* and *L* represent alleles

derived from the Wild Boar and Large White founders,

respectively; superscript *P* and *M* represent a paternal and

maternal origin, respectively. Figures with different letters

25 (superscript a or b) are significantly different at least at

the 5% level, most of them are different at the 1% or 0.1%

level.

Table 2 Maximum likelihood phenotypic means for the different
F2 genotypes estimated under (i) a model of a mendelian QTL,
and (ii) a model assuming an imprinted QTL.

Traits	Mendelian QTL				Imprinted QTL		
	$\mu_{LW/LW}$	$\mu_{LW/P}$	$\mu_{P/P}$	R	$\mu_{PAT/LW}$	$\mu_{PAT/P}$	R
BFT (cm)	2.98	2.84	2.64	0.27	2.94	2.70	0.27
% ham	21.10	21.56	22.15	0.83	21.23	21.95	0.83
% loin	24.96	25.53	26.46	0.91	25.12	26.14	0.93
% lean cuts	65.02	65.96	67.60	1.65	65.23	67.05	1.67
% backfat	6.56	6.02	5.33	0.85	6.43	5.56	0.85
% fat cuts	28.92	27.68	26.66	1.46	28.54	26.99	1.49

Claims

5

10

15

20

25

30

35

40

45

50

55

CLAIMS

1. A method for selecting a domestic animal for having
desired genotypic properties comprising testing said animal
for the presence of a parentally imprinted quantitative trait
locus (QTL).

5   2. A method according to claim 1 further comprising testing a
nucleic acid sample from said animal for the presence of a
parentally imprinted quantitative trait locus (QTL).

3. A method according to claim 1 or 2 wherein in the pig said
QTL is located at chromosome 2.

10 4. A method according to claim 2 cr 3 wherein said QTL is
mapping at around position 2p1.7.

5. A method according to claim 1 to 4 wherein said QTL is
related to the potential muscle mass and/or fat deposition cf
said animal.

15 6. A method according to claim 5 wherein said QTL comprises
at least a part of an insulin-like growth factor-2 (IGF2)
gene.

7. A method according to anyone of claims 1 to 6 wherein in
the pig said QTL comprises a marker characterised as nt241(G-

20 A) or as Swc9, as identified in figure 4.

8. A method according to anyone of claims 1-7 wherein a
paternal allele of said QTL is predominantly expressed in
said animal.

9. A method according to anyone of claims 1-7 wherein a

25 maternal allele of said QTL is predominantly expressed in
said animal.

10. An isolated and/or recombinant nucleic acid comprising a
parentally imprinted quantitative trait locus (QTL) or
functional fragment derived thereof.

30 11. An isolated and/or recombinant nucleic acid comprising a
synthetic parentally imprinted quantitative trait locus (QTL)

derived from at least one chromosome or functional fragment
derived thereof.

12. A nucleic acid according to claim 10 or 11 at least
partly derived from a Sus scrofa chromosome.

13. A nucleic acid according to claim 12 wherein said nucleic
acid is at least partly derived from a Sus scrofa chromosome
2, preferably from a region mapping at around position 2p1.7.

14. A nucleic acid according to any one of claims 10 to 13
wherein said QTL is related to the potential muscle mass
and/or fat deposition of said animal.

15. A nucleic acid according to any one of claims 10 to 14
wherein said QTL comprises at least a part of a insulin-like
growth factor-2 (IGF2) gene.

16. A nucleic acid according to anyone of claims 10 to 15
wherein a paternal allele of said QTL is capable of being
predominantly expressed.

17. A nucleic acid according to anyone of claims 10 to 16
wherein a maternal allele of said QTL is capable of being
predominantly expressed.

18. Use of a nucleic acid or fragment derived thereof
according to claim 10 in a method according to anyone of
claims 1-9.

19. Use according to claim 18 to select a breeding animal or
animal destined for slaughter for having desired genotypic or
potential phenotypic properties.

20. Use according to claim 19 wherein said properties are
related to muscle mass and/or fat deposition.

21. An animal such as pig selected by a use according to
claim 18 to 20.

22. A animal according to claim 21 characterised in being
homozygous for an allele at a paternally imprinted QTL,
preferably located at a Sus scrofa chromosome 2 mapping at
around position 2p1.7.

23. An animal according to claim 21 or 22 wherein said QTL is
related to the potential muscle mass and/or fat deposition of

said pig and/or wherein said QTL comprises at least a part of
a insulin-like growth factor-2 (IGF2) allele.

24. A transgenic animal comprising a nucleic acid according
to anyone of claims 11 to 16.

5   25. An animal according to anyone of claims 21-24 which is a
male.

26. Sperm or an embryo derived from an animal according to
anyone of claims 21-25.

27. Use of a sperm or an embryo according to claim 26 in
10 breeding animals destined for slaughter.
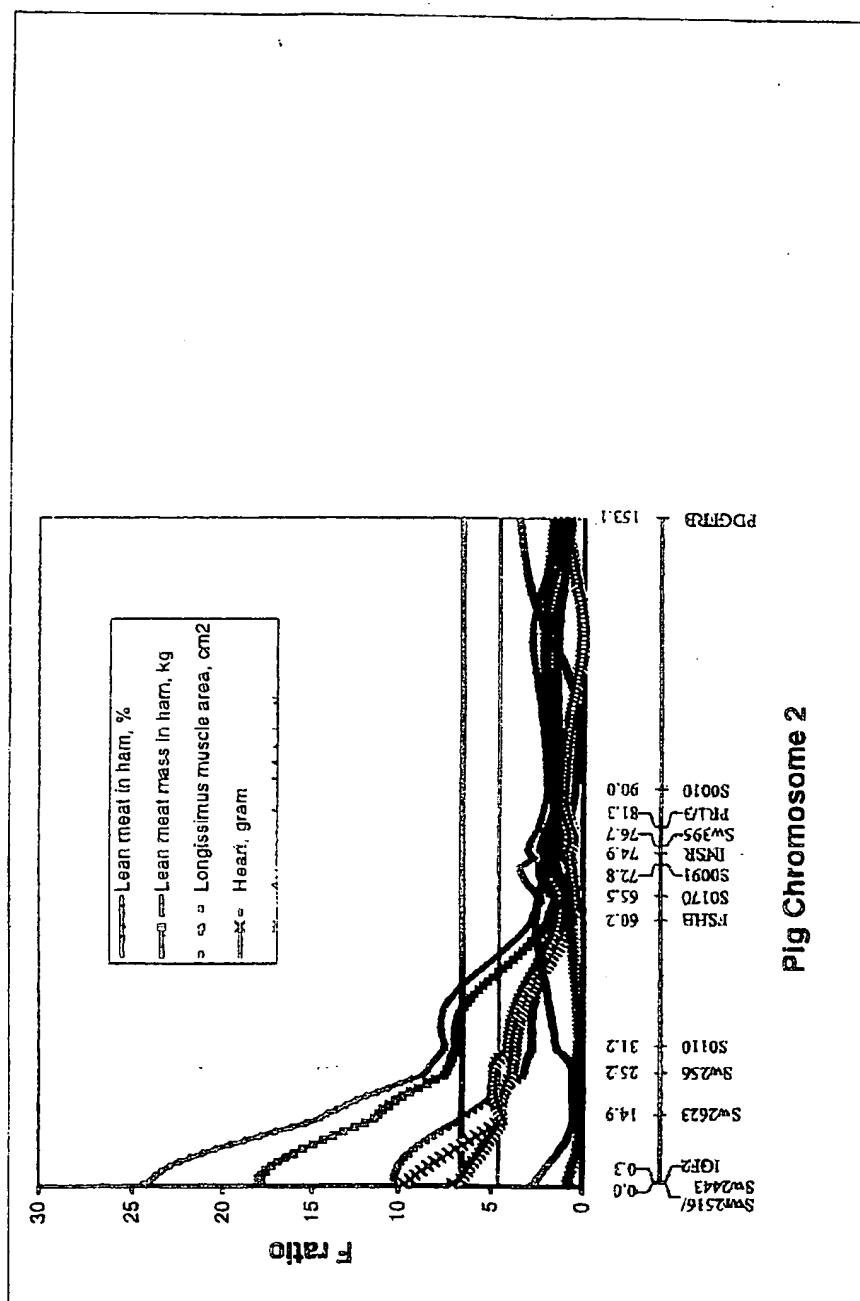
FIGURE 1

FIGURE 2

FIGURE 3A
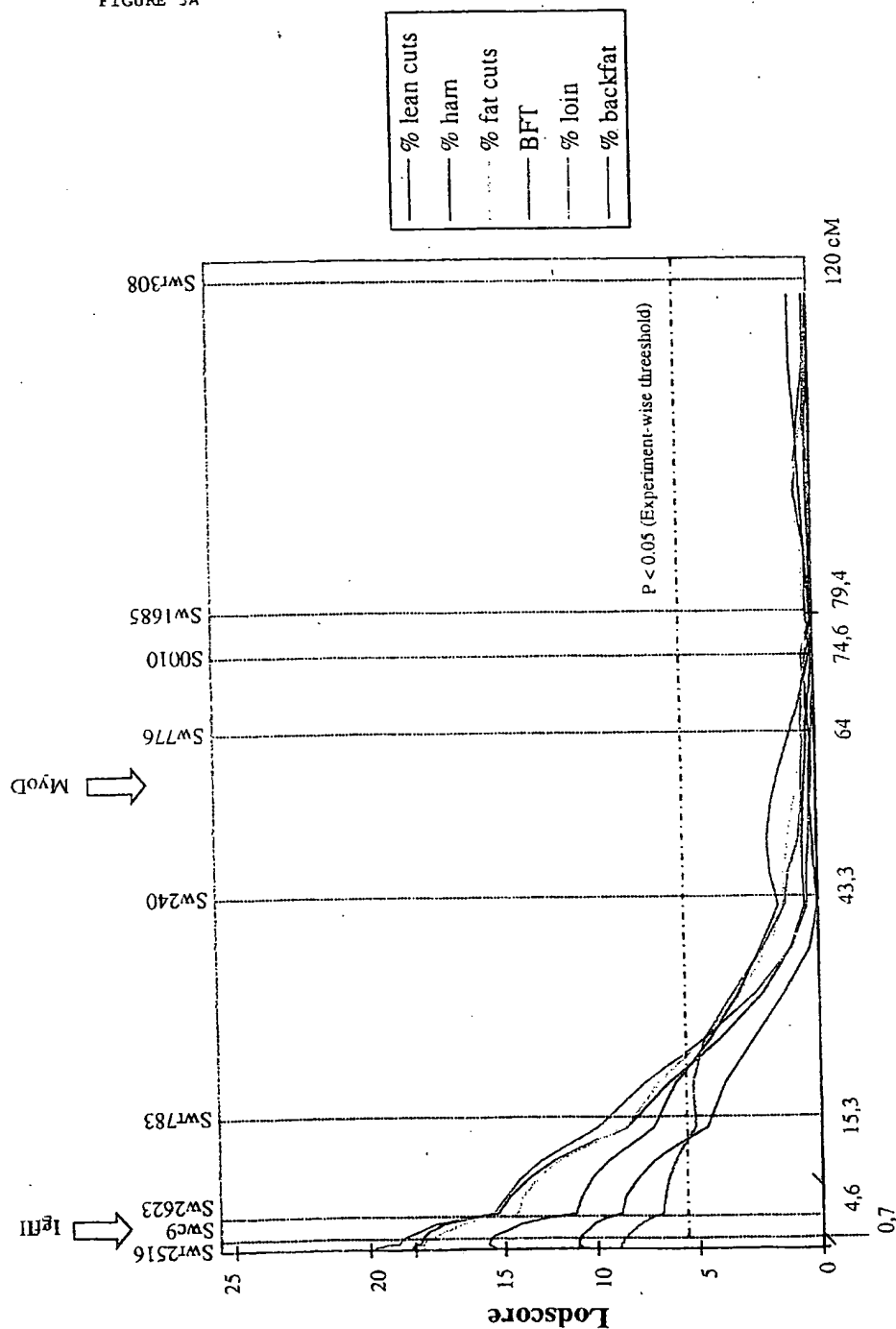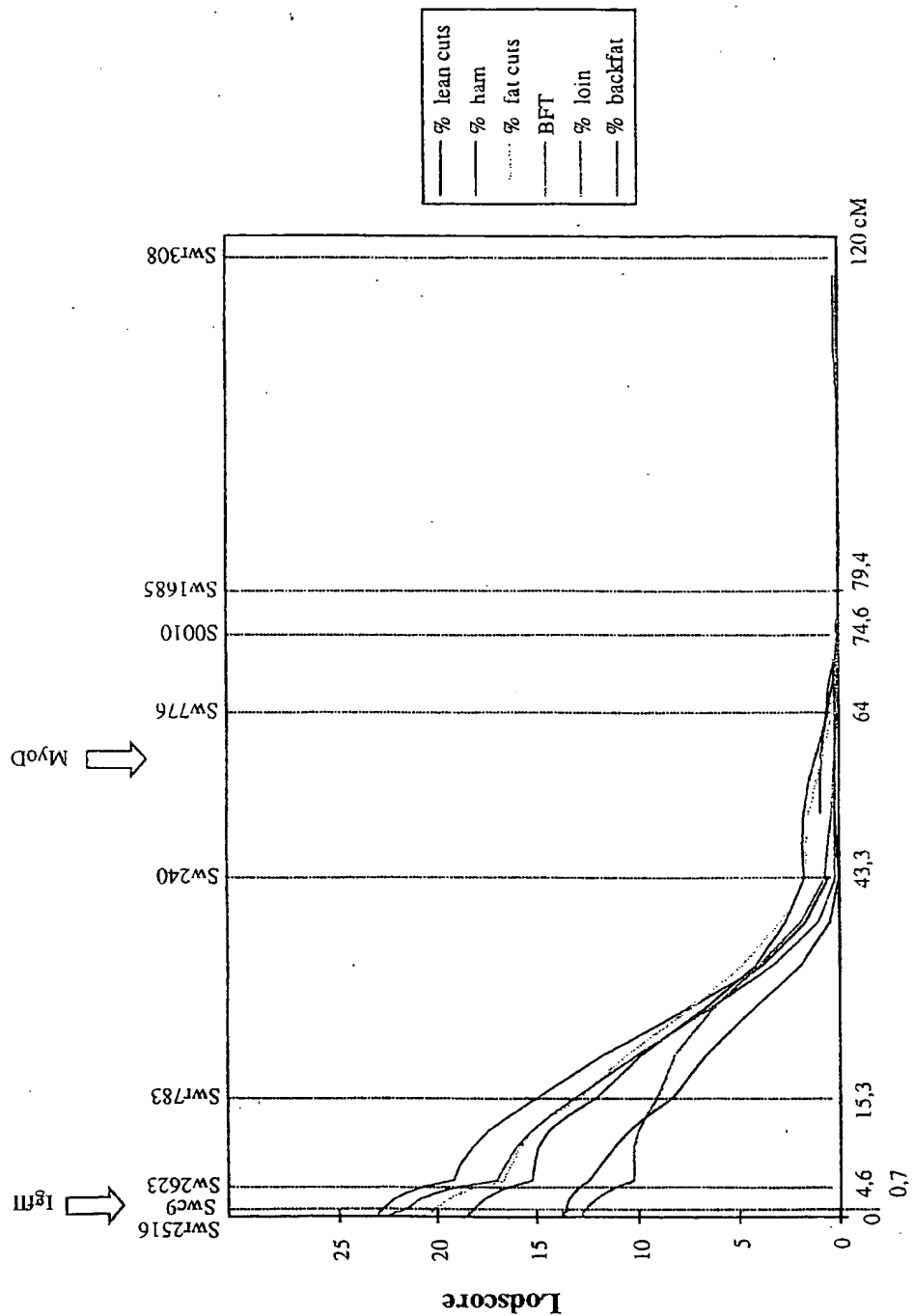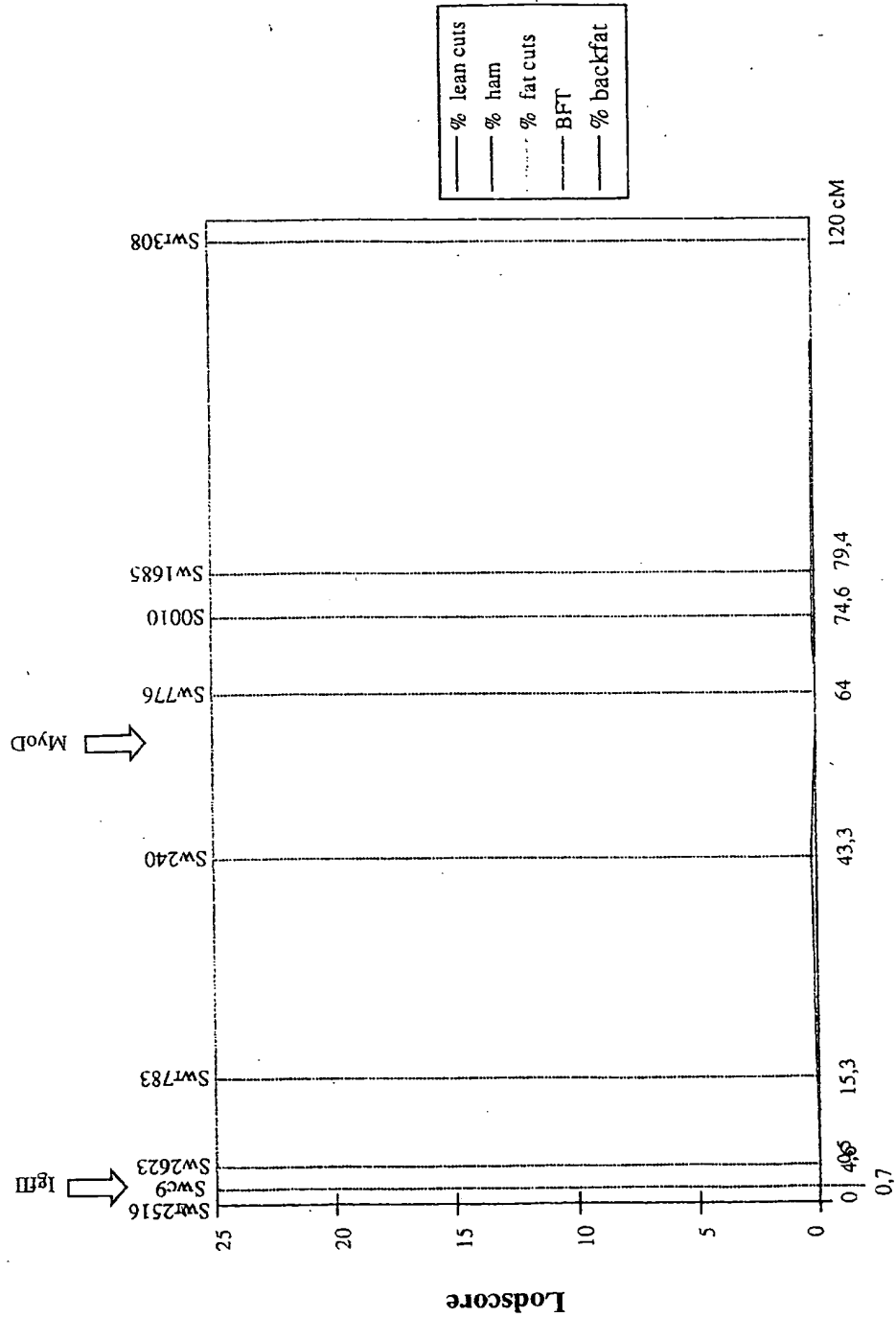
FIGURE 3B
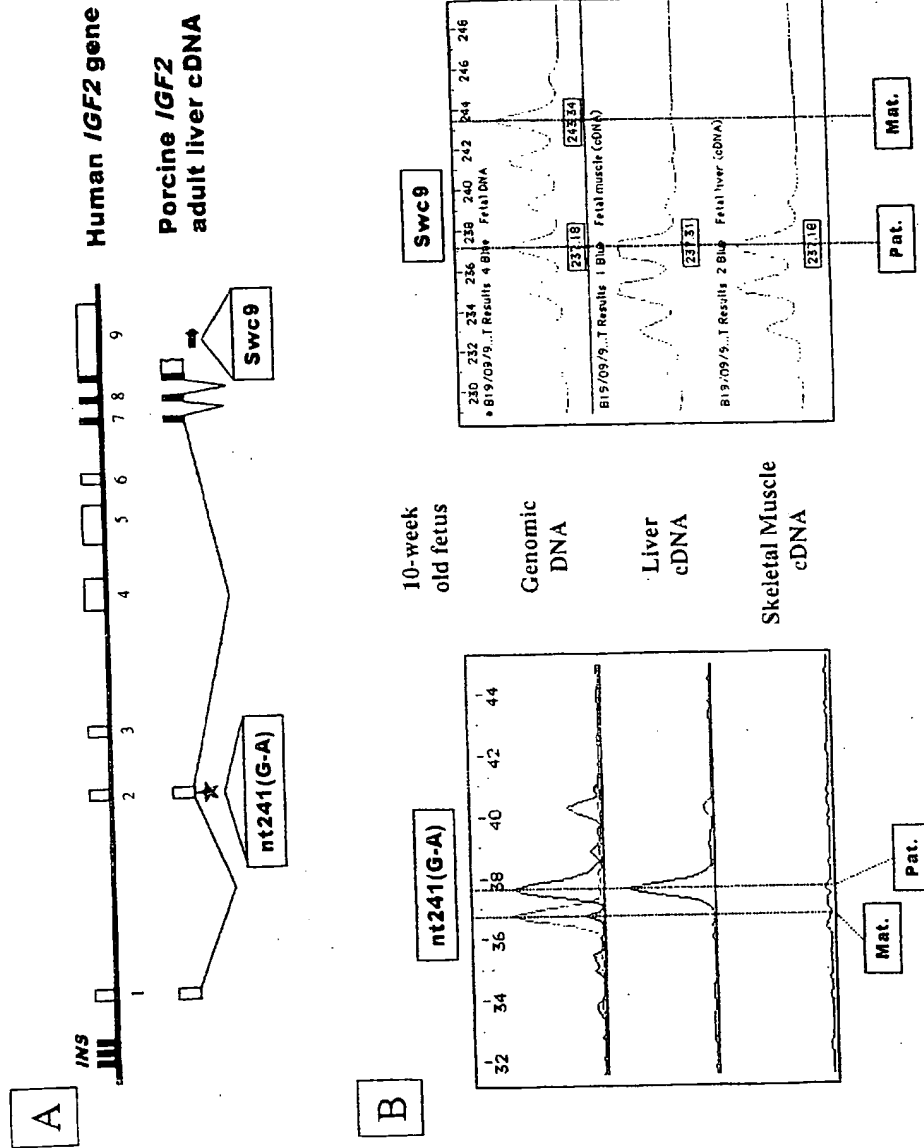
FIGURE 3C

FIGURE 4

FIGURE 5
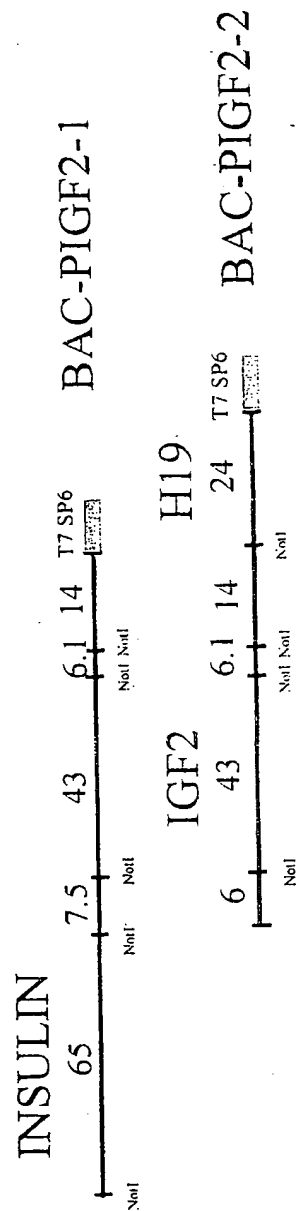
FIGURE 6

Contig 1 (500 bp)
GGGTGGGCAGCTTCCTCCCAGACCGCAGGAGGCCCAAGTTCCCTGGCCCTGCCCACCCAGGGGCCAGCTGAAGC
AGGTCAGAGACACCCGCTCCTGTCCCTCCTGTCACCTAACCCAACAGGCCGGGGCCCAGGGACACAGGCCACA
TGGCATCTCCCCCCATGCCCCTGCCCCAAGGCGCCCAGCAGGTGAGGCTGGAGCAGAGTCTGGGTCCTGCGGG
CCAGACCGAGGGCAGGACAGCTGGGCATCTGTCCTCACAGTCCCCGCGCTTTGTCGGGAGGCGGCAGAGCCTC
ATCCAAGACGCCCGCAAGGAACGGGAGAAGGCGGAGGCCGCGGCTGCCGCGTCCGAGCCCGGGGAGGCCCTGG
AAGTGGGGGCCCTTGCCGAGCGGGACGGGAAGGCCCTGCTGAACCTGCTCTTCACCCTGAGGGCCACCAAGCC
CCCCTCGCTGTTCCGGTCCCTGAAAAAATTCTAGGTGAGGGGGCGGGCCAGGGCTCCCCGGG
Contig 2 (943 bp)
TGCTCCTCACACCCCGGGCGGGGCTGCTCTTGGGGCCATCCTCCCCATGGGCCCAGCACCCACTCTGGCCTTC
ACACCTGCCGTCTTCTGGGAAGTCCTCTGGTTCCCAAGGAAAGTTTCTGAGCTGGACAAGTGCCACCACCTGG
TCACCAAGTTCGATCCTGAGCTGGACCTGGACCCACCCGGTGAGCCGGTGCCTCCCCTCCCCGGCCGCCATGTC
TCCCATCCCCAGGGGTGTCCCCACACTCAGGGCCCGGACTGGGCGTGAACCCCGGGTTGGGACGGATGTTGGC
CTGCTGTGTGGCCTCCTGGCGGAACAGAGAGGCCTGGCTGGGTGCCACCCCCAGGGCCCCCGCCGATGACACGG
GCCGCGTCTGGGCTGGGCGGGCAGGGCGGCCAGGC
AGGGCAGCCTCCGATGGCGTCCCCGGCTGTCACCAGGGCTTCTCGGACCAGTTGTACCGCCAGCGCAGGAAGC
TGATTGCCCAGATCGGCCTTCCAGTACAGGCAGTAAGTCCCTCCAGGGCCTCAGCCTGGGGGCCCAGACCTCAG
CCTGGGCCTCACGCCAGACCTGGGGGTGGAGGGAAGGGAGGTTGTCTTTGTCACCAACGCCACCACCTTCACT
GTCACCATGGTCACCGACTCTGGGTCCCCAAATCACAGCTGAGGAAACTGGGGCACAGAGTGGTTAAGCATCT
TGCTGAAGCCACACAGCTGGCGGACCATTTGGCCCCGGCCCCTCCTGCCGGCTCCCACACGTGCTCCCTGAGGG
GCCCGGGACTGACAGCTGTCCCCTCCTCAGAGGTG
ACCCTATTCCCCGCGTGGAGTACACAGCCGAGGAGATTGCCCACCTGGTGAGGCCCTGTGACAGCGGCTGGGAG
GGGCGGGAGTGGGGGAAGGGACAGGAAGACCTCAGAATTCCCGCGTCGAACGTGGTGGCCTCTATCATGA
Contig 3 (1500 bp)
GGGGAGGGGATGCTCAGACCCGCTCTGGGAAGAAGAGAGCCTCAGAAGAAATCCCTTCCCAAGGGTCACGCGG
TGGAGCCCAGGGGCCCGCTAGCGGCCCGATTCCCACAGCTCGTGCTGCCCACCTGCTGGCGCTCCCAGGAACTGC
GGAGGCGGTGGGGGCCCTGGATGGGTCCGGCAGTGGGCTCGCAGGAGACCCCTGGAGGGGCTGCGGGACACCCC
AGCTGCCACTCACAAGGTGCCCAAGCGGCGGTGGCAATGGGCTGAGCCTCTCCCCCCCTCCTCCTCCGCAGGA
CATTGGCCTCGCATCCCTGGGGGTCTCGGACGAGGAAATTGAGAAGCTGTCCCACGGTGGGTTTCTCCCCCTGC
AGGGCCCTGGGTTCCAGCCAGGCCCTCCTGTCCAA
GGGGTGTCGTCCTCACGCTGTGACCGCCCGGGGAGCCTGGATCGGTTCTGCCTGGGTGGGCGGTGCCCGGGCCA
CGGGCAGCAGGGGCAGCGGTGCGGGCCCCAGCCGTGTCTGAGCCCCCTTGCCGCCTGTCCCCACCAGCTGTAC
TGGTTCACGGTGGAGTTTGGGCTCTGCAAACAGAACGGCGAGGTGAAGGCCTACGGGGCTGGGCTGCTGTCCT
CCTACGGGGAGCTCCTGGTGAGGCCTCCCCACGCGCTGGGGCCTGGGTCCCCGGGGGAGGTGACCCCTGCGC
TGCCTTCTGGATTCCAGCTCTCGGGGAGGCTGGAGCGAGGGGCTGCCCTCCTGGGGGCCACCAAGAAAGCTGGTC
TGCGCCCCTCTCCACACACCTGTGCCTGGGCCCTG
GGGGGACCCCTGCTGGGGGATGTGGGTGCACAGCCAGGGCCACCAGGGAGTCAGGACACGGGGCTCCCTTCCC
TCGGGTCCCTGAGACCCCTGGCCTCCCGCCAGCACTCCCTGTCCGAGGAGCCCGAGATCCGGGCCTTCGACCC
CGACGCGGCGGCCGTGCAGCCCTACCAGGACCAGACCTACCAGCCCGTCTACTTCGTGTCTGAGAGTTTCAGT
GACGCCAAGGACAAGCTCAGGTGGGCCGGGGGCCGGGGGCCCCAAACTGGAGGATCCAGCCTGCAGCCCCGCC
TATGAGCCCATTTCCCAGCAGAGGGGAGCTGCTGCGGACCCCACCGTCACAACCCCCCTTCCCACAGCTGGAACC
CCAGAAAGCCTGCCGGAGGGGGGGACCTGCAGGGCTG
TGGCCAGGTCGAAGGCCAGGTCGAGGCCCAGGCTTTTAGGGGTGAAGTCTGACTTTGTAAGAGGCGGGTGCAGGGT
CCTTCCCAGCCTCCTCCCCTCCGAGCAGCTGGGGGCGGGGCGGGGGTGCGATGAAGGCAGAGATGACGCAGCC
ACCCGTTCACCCTCAGGAGGCGCCTCCTGTCCAGCCAGGCTCCTGTTGTCACAGGGGAAACTGAGGCCCCAGG
TGTGTGTGTGGGGGGGTGATTCTCACACACAAGCTTAGGGACAGGGACATAACGGCCTCTCCAGGGCACACAG
TCTGGAGG
Contig 4 (3024 bp)
TTAANTCCANGTTGGCCCGACAAGTTTTCCCCATTTGAAAAGGGGGCCAGTTAAGCCCCAACNCAATTAATTGG
AAGTTAGCTCCCCTCATTAGGCTCCCCAGNCTTTACNCTTTATGTTCCGGTTCGTATTTTTGTGGGGAATTGTA
GCGGATACAATTTCTCTCAAGNAACCAGCTATGCCCATGATTACGCGGTACAGTAGTTCATCAGTCCCCCCCG
CCCATGGGACAGCGAAGGGAACCAGTATGTCGTGGGGCCGGGTCTAAAGGGGTCACCACCAGGGAGGGGCAGG
GGCTCCAGGAGGCAGGGCCACTGAGCGGTACCTGGTGGGGGGGAGGTGGTGGGGCGCACACCCAGGAGTCCTGTG
CCCCCCCCACTCCCGCCGTTGGACATGAGAAGCAGGGGCCAGCCTGCGGGTCCCTGACTTCAGCGCCCCCCCC
CCCCACCGCCGCAGCAGCCCGGGGTCTCAGCAGGCTGCTGTGCTGGGGGCCGGGGCGCTTATGGRGCCGGGAG
CAGCCCCCCCCCACGGCTTCAGAGCATCTCTGGGGCCTCAGGGATGGACCGGGGTCTGCRGGCAGGTGTCCTC
TCGCGCCCCCACTCCCTGGGCTATAACGTGGAAGATGCGGCCCAAGCCCGGKCGGTTTGGCCTTTGTCCCCAG
CCAGTGGGCAGCCTGGCCCTCAGGCCGCTCGTTAAGACTCTAATGACCTCAAGGCCCCCAGAGGCGCTGAT
GACCCACGGAGATGATCCCGCAGGCCTGGCAGCAGGGAAATGATCCAGAAAGTGCCACCTCAGCCCCCAGCCA

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCTGCCACCCACCTGGAGGCCCTCAGGGGCCGGGCGCCGGGGGGCAGGCGCTATAAAGCCGGCCGGGCCCAGC
CGCCCCCAGCCCTCTGGGACCAGCTGTGTTCCCAGGCCACCGGCAAGCAGGTCTGTCCCCCTGGGCTCCCGTC
AGCTGGGTCTGGGCTGTCCTGCTGGGGCCAGGGCATCTCGGCAGGAGGACGTGGGCTCCTCTCTCGGAGCCCT
TGGGGGGTGAGGCTGGTGGGGGCTGCAGGTGCCCCTGGCTGGCCTCAACGCCGCCCGTCCCCCAGGTCCTCAC
CCCCCGCCATGGCCCTGTGGACGCGCCTCCTGCCCCTGCTGGCCCTGCTGGCSCTCTGGGCGCCCGCCCCGGC
CCAGGCCTTCGTGAACCAGCACCTGTGCGGCTCCCACCTGGTGGAGGCGCTGTACCTGGTGTGCGGGGAGCGC
GGCTTCTTCTACACGCCCAAGGCCCGTCGGGAGGCGGAGAACCCTCAGGGTGAGCCGAGGGGGYGTCCCGGGA
GCGGTYGGGGGAGTTTTTAAGGAGGAAATTGGTAAAAGTGACCAACTCCCTGGGAGCTGAGCCCAGAGACACC
CCTCCCACGCCCYGGTCCCGCTCGAGAAGCCCCCCTTCCCTCCCCTCCTCCCG

AGGCGGCTCCAGGGAGGAATCTTACGGAGTCAAGGCCCGGGTGCCGCTGGTCTCCGAGTGACATCGCCGTGGT
GTCCCRTCTGCCGGCCCACATGCCCGTGAGAGAWGCCCCATCCCCCTGGGAGGCGGGCCCCGTGCCGGGCAGGC
GGCGGGAGGCCCAGGACCGGTGGCTGCTCGGCTTCCACTCCAGGGTGGGCGGGGTGGGGGTGGCTGTCTCT
GTGTGACCGGCTCTCCCCCGCAGCAGGTGCCGTGGAGCTGGGCGGAGGCCTGGGCGGCCTGCAGGCCCTGGCGC
TGGAGGGGCCCCCGCAGAAGCGTGGCATCGTGGAGCAGTGCTGCACCAGCATCTGTTCCCTCTACCAGCTGGA
GAACTACTGCAACTAGGCCGCCCCTGAGGGCGCCTGCTGCTCCCCGCACCCCAAAACCCAATAAAGTCCTGAA
TGAGCCCGGCCGAGTCCTGTGGTCTGTGTGGCCTGGGGCCGGGGGCCCTGGTGGGGGAGGGGCCAGAAGGCTGT
GGGGGGCCTGCCTGCGACCCCTCTCTGCTCTCGCCACATCGGCTGCTCTAAGCTTCCTCCACATGCATCGGGT
GCCCACAGGCACATGGCCACCGGGGGACCAGGGCCCAGGGCAGGGCCCTTCAATGTGGCGAGCTCTGGTTTTC
AGGGCTCCAGACACCCCCTCCTGGGTGCCCACTGCTGCACAGGGTCACTCTGAGGGTCACAGGGCACCCACCC
AGACTGCTCTTGGGCACACAAAATAGCCCAGGGGCTTCTTGGGCTGGCTGCRGTCTGGGAGGTCAGAGAGTGA
CCCCGCGGGACCAAGACCTGGCCAGCCTGCCAGTCGCCCAGGCCAAACCAATCGCCACCTTTGCTGAAGGTTC
CACCCGGGCCAGCACTGGGGGCGGCCGGGCCTAGAGCTGGGCGCCCGGGCCCCAGGGACTGCACACCCGCCAG
AGGTGGGCCTGAGGGGTGGCAGCAGGCCTCCCGCCTGGGACCCAGCCAGCTGGGCAGCTCACCTCTCAACACG
AGGCTCTCACCTGTGTCGTCCCCTCCCCACGGCCACACAGACACCCCTGGGGAGAAGTCACAGGCCCCCAGCA
GGCCCCGCCCCTGGAGAGGAGGCCAGGGCTGGGCAGGCGGGTGGCCGGCCGGACACTGGACCCGGAAGGGGGG
TAGGCGGCTGGGATGAGTGGCGAGCTGTCCATGGGAGCACCCAGCGGCCCCATTGGCACCAGTACAGGCAGGG
GCACCTGCAGCAGCTGAGGTACGTGGGGTCCCCGGACTGGTTGGTGTCCGGCTGCCCTCTGGGAGGCAGCGGG
CTGAGCTTGTGGTCCTGCCAACCAGGGAGACCCGTGACCACCCTGCTGCTTCCCCTCCCCCCCAGGGCCAGCA
GACTCCTTTGGGACTCGGGGCCCCTGAGCCGCCCCCACTCGCAGGACTCACCGCGGCTGTGCGGTCCTGGGTGAG
TGGGGGCTTGGGAGAGGGTCACTCTTGTCCGTCGGCTGGGGAAGGCTGAGAGTCATGGTGTGACAGCGCCCTC
GGCCTGCCGGGTGGGGGGTCTCCCTTCTCCCGAGCCCAGATCCCCGGGTAC

Contig 5 (1730 bp)

CGTCACCCGCAGAAGCCAGGCCCACAGGCCTTGGCTCAGCCCCTCCACCCAGGCCCACGTTCCGCCCCTTCTG
GGAACTGGAGGACAGCCGCCCTCGCCCTCGGACCTGGCTTCGTTTGCCCTGGCATCTGGCAGTGGCCGGCAG
CTGCGTTCAGCCCCTGGATGACACCCTGGCGTGAGCGGTGGGTCCCCGTGCTGAGGGCAGCCCCCACACACGTC
CTGCTCACTTGCCTTGTGTCTGCTCCGCATCCCGTCATCACACATGCCATGCTGGGGCACCGTAGCGCCTTGC
CCTGTGTGGCACTGTGGCACTGTGTTCCTGATGGGAACACTGAGGCTGGGGTCAGGCCCGCTGCTGCCCACCC
TCTAAGGACATTCTGCCGGTGCAGCTGCCTCCAGG

CTGGCCCCCCGGATTGCATCTGCTTCTGGCACGGATGAACTGGCACCTCTGCCTGACCATTAGGGCTGTATTT
GCCTTCTCCTGTTGGCAGTAAATATTTACTGTCCCTCCCTGTTCCTCCAGGCCCGANCCAGTTCCTGAGGGGC
ATGGGAGGTGGACACAAAGGTGCCCAAGCAGCCCCCTGCTCTTGAGGGCCCAGTGTCTGGTGGGGGGCCAGCCT
GGCAAGGAGGAGCGAGACTAGGAACCAGAGGCCTGTGTTCCTGGAAAAAGGCCCCCTGGCAGAGTTCCGGCTGG
TGTGTGTCCAGCTAGGCTGTGAGTCTTCAAACTGGGGAGCCCGGCCCCTGGACCCAGGCAGGGCTGCACCCCT
GGTGCCAGTGCTTCACTGGGTGGGCACCTGTCCCC

ACCAGGCAAGGTGGTCCGAGCGGTCATTCACAGACAGAACCAGCAGAGGGCGCCAAAGCCCCACTTTTGACAA
ACTCCCCTTCGCCCTGAGCCGAAAGTCCAGGCGGCAGGTGGACCTCTCTGCAGGGCTCTGCCACCCCTGCTGC
CGCTTGCCAGCACTCACAGCGGCTGCGGGGGGTGCCCAACAGGCCGGCTACCCTGAGCTCTGGAGGCGATGGA
GTTTAGGAGGGAACGAGGGGACTCCTGGGGGTGACTTTCTTCAGCGCCCACATTGCGGCCCAGCAAACCGAGG
CTGGAGGAGGCCGGGCACCTGTGCCCAGCTGGAGCCTTTGCTGAGGGTCTCCAAGGCCTGGGGAAATTGAGGC
TGGGGGCTGGGGGGTGTCACTGTCGGGCCAGGAGG

CCCCTCGCTCTGATTGGAGCCGCCTCGGCCACTTGAGCCAGGAGGCTCACATGAGGCGGGGGCTGCAGGGACA
GGACCCTCGGGGCCCGGGAGGCCTTGGAGGGGGTCCAGCTGGGCCAGGGTTCGTTCTTTCCCGGGTCCATGTC
CACCGCCCTCCCGCTGCTGGGAGGAGAGGAGGTCCAGGGCAGAAAGAATGCGTGGGGATGGGGGGGTGGTCAG
GGGTCTGGGAGCTGTGGAAACAACAAACAGACAGCGAGGTCCTGGGGCGCCCGGCCCCCCGCCCCCTCCGGCA
CTGTTGTTTCTGGCCGGGGTGCAGGGACAGCGAGGCAGATTCCTTCGAAAGTGGAGACTGGCGGGGGGGCCCCT
CGGGTCCTCAGCTCACCCCCTGAGCTAGCCCGCCC

ACTCGGCTCCAACCTCCCGCAGGCCCCTGGCACGGTCTCCAGGAGTCCACTCAGGGGTCCCCAAAGCTGCCAC
CAGGAGCTGGGCCTGGGTCTGTCACCACCCCACCCCACCCTCCAAGTCTGAGATATG

Contig 6 (4833 bp)

ATGTGAGCTGCACAGCATGAGCCCTCGGCCCCACTGCTGTGGCCTTGCGGACATTGAGGTGTGTGCCGCCCAG
GGCGACCACACCCTGGCCTCTCAGGGTGCCCGTACAGAGGCGGCTGGGTCGTANGAGGTGCGGGGGCTCTGGGG
ACCGCTGGTGAGTTCAGGACGGGGGTCATGCCACCTCCTCTCTGAAGGTTTGGTGAGGTGGCCCTTCTCTTAT
CGTGATGACAATACTGATTTCTGGAAGAGCCAGGTGTTTTCTGAGGCTGTGGTTGCACTTCTCCACGTGGCCA
CAAGGTGCCGGGCTCGGGTCAGATTTGAGAAGCCCTGCGGGAGCGGGTGTCATGCGCCAGATTCAGCTTGCCT

FIGURE 6, CONTD.

```
CCTGCGGGTCTGGGGTCAGGACGTGGTCCCCAGCAGTCTGCTCCAGAGCCTGTCAGTGATGTGTGGGATTTTA
CCGCTAGAACACAGTTTCCTCTGATTCTCAGAAACCAGCAGATGCTTTAGGAGGGGCGTGCAGGTTTCACCTG
TGCTGCANNGCCCCCTGCCACCTGGTCGGAGCCNCAAGACGGCATCTAAAGATCAGTTCCTCATCATCAGTTC
CGCAGTGCTGGGGTGGGGGCAGATGAGAACCTCAGGGCTGGGCGCAGAGGTGGGGAGCCCGCCTGGACCCCGA
CACTGCAGGGGGGGCCTCCCCCTTGTAGGAAGAACAATGTCGCTTTGCCCACCCAGCCCTCTCCCCAGGGTGCCC
CGAACTGTTGCTCCTAAGACCTCTGGGCTGTGTGCTGTAATTCTATAAGTGGCCACCAGGTGTCAGCAGGAGG
CCACTTAAGCATCCATGTGGCGGAAACCTGGAGCTGGGGGTTCCTAAGGGTCCCTCGAGTGTCTCCTGAATAA
ATAGGCGCTGACCTGATCCCCAGGAAGGGATAACCCTCTCCCAGGCCTAAGAGGCAGTGGGGCAATGAGGTTT
ATGTGTCCACTGTACCCCCAAATTGTCTCTTCCTTCCCTCTACCCTGTGTCCCCACCGTGGACGATACACGGA
GTGCCGAGGCTGCGGGTCACAGCCCTCACAGCCCCAAAGCTGCAGGTCCTGCCTCAGGGGCACCGCAGCTTGGC
TGGTCCCCCTTGGGTCCTCCCCACCCTGACCCGTCCTCTGCTCCCCTCCCTTTGCTTAAATGCTCTGCGTTTC
AAGGTTCTGATGGAATAAAATAGCCCTGCACTGGTGTGTTCCTCTTTGGGGCTGTGCCAGAAGTGGGAATTCA
GACCAGGGCAGAGCTCAGATTCCACATACTGTGTTAGGGATGGCAGGTGCCACATTTCCAGGACTTTCATTGG
TGGTTTGTAAATGCTACTTCCGTTTCAGCCCCTCAGCTGCCCACCTCCTCAATTTAGGGACCCCCCCCCTTTGG
CGGGTTGCCCATGGAACCACATCATCTGGCGTGGGGTGAGCCCTTTATCCTCCCTGGCCCCACTGGGAGGGTT
TGGGGAAGTCCCAGCTAAATTTCTCCGTAGGGACCTGGAAGGAGCCCTTGTGACATCTGGGCACAGATAAGAG
GTAGGGGGCACAGGCCGTGAACACTTGAAGCTGCAGAGCCCAGAGCAGAGCCAGCAGGAGCAAGTGACTGCTC
CCCACCCCAAGAACTGTGGGCTGCGTCACACACTCCCCACTGTGTGCCCTGGACCTGACAGGGCCTTTAGCCT
CCCTGCATCCCTCCCCACCCAAGAACCCAGTGAGGCACCCCACTTGCCCCTCCTTAGTGTTGTTATGGCTCTG
GGGCATCTGCATTTTGTTTAGGACACCCCCAGCTAGATTTAAGTCCCCCCAAGTGTGACTCTTTCCTCCACTG
AAAACCCTGTCCTCCCACCAAAGGGCCCTATCCCTTTAGCTGAGCCAAGGAAATTCAGGAGCGGCCTTGAATG
ACAAAGGAAGAGGGGGAGAGTTAAACCCCAACACTGGCTGGCAAGCTGGGTGGGGTGGACACCCCAGGGTGCA
GGGGTGCAGTGAAGGTAGCCGCTCGGTGGCCTTCTGGAAACTACATGTGACTTTCCCATTAGGTGAGTCTTTGC
TTTGCCCCTGCTCTATCTGCAGGCTTATGCAAGAAGTTTAAATTCCCAGGGACACTTGGTCTAACCAGGCAGC
GCTTGTATCTGGGCCCTTCCCCAGCTGCTGACCACTCTGAGTCTGCGCCTTAGTTGGAGTTTTGGCCAAGCTC
AAGAGCCTGTGGACCCCAGTCATCCCACCCAGGGGTGCCTGTGGGCAGGACGCTGCTGCCTGCCATTTGCTGC
AGTATTGTCACTGTCCGGCACCACACACATGGTGCAGGGGGTGGTATCAGGTGCCACTGGGCGAAGGGAGCAAAA
CTCCCAGGTGAGTCCCCTGCCTCTGGAAGCAAGATGCACATGACCGCACTGTGTTGCAGCTGCATTGGCAGGG
CCCCGAACAAAGATTTTTCTGATCTTTCTCGAACCCTGCTTTTCCCCATCATGCCCCGCCCCCATTTTACCCGT
GCCCACGCCCACTGGTGTGCCGGGGTGTCAAGTGACTGACAAGTGTCAATCTACTGAGGCCCTGCCCAGTCTCC
ACCCCCCACATAGTCCCACCTCCCAGCTGGCAGGGAGAACTTCCAGCTAATGCCCATGCCCACAAATGTCTT
TCTGTCAGCCTAGAGCTGGACCAAATCTCCACCCTGTAACATGCTGTGCCCTGGCGTGGGAAGGTGCCAGAGC
CAGTTGCCCCAGCAGCCCCAGAACCACTAAGTTGGCACAAAGCTACCCAAATTTGGAGGGGCTTGGGGAAGGG
CATGGAGGGGATGAGGAGGTGAGGGGCAAAACTAATTTCACTTAGCCATTTGAGCAGGTGCCACGCTCAGCGTG
GAGAGGCTCTCTTGCTTCTAGGGACCCATTATGATGCACGCTAAAAGCGCCCTTCACCATCTCTCCAGCCT
CAGCTTTGTCCCCCTCCTCCTCCTCAGCGGCAACCCGGCTGGAGGGTCTGGCCACTACAGCCAGAGCGCCCCC
TACTTTGGTGGCGACTGCTACTATTGGCCCAACCAGCGGATCACCGGCCAGGCAGTTCGGCAGAGAGTCTGG
GGCACCAGTGACTCCCCCGTCCTCTTTATCCACCACCCAGGAGCTTCAGGGACTACACAGCGACTAGAGGGCA
GGTAACTGGTCTGCCCTCCCTAGGGCTGCCCCCTCAGAGTGTGTGAGAAAAGCTGCATTGAGTGTTTGGGTGC
AGGTGGGCTGGGGGCTTGGGGCAGCCAACAGGAACGGCGGGACCTCTGCTTCCAGAGGACCCCAGATCCTGGC
AAGCTTCGACTTTGGAGGGGACAGGAAAGACAGGTGGAGAGGGGACACTTCCCTCTTCGTACAGACGCCCAC
CCGGAGCCACAGAGGCTTTTGCAAGGAAAATAGGTTTTCCCTCACTAATGCAGCAGGCAAAATGGGAGGGCCA
GGGGTGGAGGGTAGTGCCCCCGCCCCCAGCAGGAGGGCACAGCCTGTTTCTGCAAATGTAAAAAAGCAGGGTTT
TTCTGTGTGAGAAGTTCCCTCTTGCTGCATGTCCCCACCCCCGCCACCAAAGACAAACAGGACACTGTGCAGA
GGGGCCAGAGCCCCGAGATTTTGGAGTTGTTTTTATATGCATATATACCATTTTGAAAGCAAAGCTTCCCTCT
CCCCTACTCCCTACATGTCCCCCTTCACCAAAAAATCCCACCACGTAACTGGAAAGGGGGAGTGAGAAGGACGA
CGAAGGGGCACTGTCCCCTCCCGTCCCACAGCGGGACTTAAAACGTACAGCTTTTCGCCTCCGGACAGTGTGC
CGCCCCCTGGCCCCCGTCACGCTCCCCTGCCCGGCGGGGCTGAGTGTGGGGCCAGGGCCTGTCTCCAGGCATGC
ATTATTTTGTGCATGAAGGTTTTGTCCCGCCCACCCAGGCTGGTGTTGGGGGGAAGGGGTTCATTGCTCCAAA
GAAGCCCATCTCCCCCCTCAGCCACCTTCAGCCGCCTTCGCAAGGCAGAGCTGTGTCCTCTGCTGTGTGCCTG
GCCCCCTCCTTGCTTCTATTCAAGGTGGAAGTGTTGGGGGGAGGAGAAGAGTTTTTATATTGTGTCTGTGATC
CCCCGAGGCAGGGCATTTGTGTGCGGCCCCCCAGCCCCCAGGCCCAGGCAGATGGGCCAGCCTGCCCGACAGA
AGGGTCTCCTGCTGCTTGGCTGCAGGGAAACCCAGCTCTGGGTGAACCGTGGGCACCTTCCTTCCTCCATGCC
CTGTATTTAAAGAAGGAGAGCTGGGGGGCCAGAGGCACAGGGAGGGGAGCCACGGCCCCAGGTCTGACAAGAT
GACCTGCGGGCCTCTCCACCCAAGAGTCGGGGTGGGGGGGCGGATTTGGTTTGAAAAGAGAACAAATAGGAAC
ACACTCTTTATTTTCCCCAGGGGCCGAAGAGTCACCCCTGAACTTGAGGACGAGCAGCCGGATTCCAGCCCCC
AGCCCCAGGGCCCCACATCTCCTCGGGCTCAGCCGCGCGCCCCAGCTGCCCCCCAGCCTGAGCTGCAGCAGGC
CAGGGCTGCCCGAGACCCCAGCCCCCAGGTGAGCTGCTGCAGCCTGTGGCCCAGGAGATCTCCGCCGGCTCAG
AACTGAGGCGGGCAGCCCACCCAGCCCACAGCGGTGAGTGTCTCCAGACCCCAGGGCAGGGCCCGGTGTCCCC
CGGCACAGAGAGCTCGTGCTGCAGGCCCAGACCTCCCAGGCCGTTTTAGTTCCCATCTCCCCTTGGGGGAGGGG
TGGGGCTCAGAGGGGGCTGGGGTGCATCCGCAGAGCTGGGGTGCAGGGCTCCAGGTGCCTCTCTCCCAGGCGGC
TGGCCCGGAGGGGGG
```

Contig 7 (2014 bp)

FIGURE 6, CONTD.

CTGGTTTCGCACTCCTCCGGGGACTGTTGAAGTACCCGAGAGCGCNCGCGGAGCGCCGGGGCGAGCGGGGGTG
GCCGCCGGGGGTGCTCCCGGGCCCCCGGACCGAGCCAGGGACGAGCCTGCCCGCGGCGGCAGCCGGGCCGCGG
CTTCGCCTAGGCTCACAGCGCGGGAGCGCGTGGGGCGCGGCCGCTGCCGGGAGTCCGCCTGCCTCCTCGGAGG
CGGCCGACCGGGGAGCCTGGGGGACCCCGAGCGCGCCCGGGGAGCAGCGCCCCGACACGCCCCGGGCCGCTCTCG
GCTTCCTCCCTTCCAGCCGGCGCCCGCGCGGCCGGGCTTCGGCACCGGGGCGCTCTCAGTGGCAGGAGAAGCG
TGCGCTCCCGCGGGGTGGGGGACCCGCAGGAAACC
CGCACCGCCTGGAGCCGCCGCCGCGCGGCCAGCGCTCGCGTCCCCCGGGGAGGGCGCCACTGCTCCGCGCGCG
CGTCCCCCGACGCCCCGCGCGCTTCCCCGGCCGGCCCGGGATCCTAACCTCTCTCTCGGTCGCAGCCCCGCAT
CCCCAGGGCTCCAGGCCCCCCGCGACTTGCCCGCTCCTCCCAATTGCAGACACGACTTTTTCTGGGACCTCCC
AAAGGACAGCCTGGCTCCAGGGTCCCCCAGATACATTCACCATTTCTCCAGATCACAAGTGGGTTTTTCGGGC
ACTAACTTCCAGAGACCTCAAAGCACATGAGCCCCTACTGGCTTTCCCAGGTTTCCACTAGTGGCCTCGGTCC
CCACCTCACTGGGCATTGTCTCCCAGGCTCTTCGC
GGTGTGATCCCACCCATTCGCGCCCAGGTCCCGCAGTGCCAATCCCTCCTCTAGAAAACTTAAACACTGACTC
CTGGTCTCGGGGTGAGGCTGCCCAATGTGCCTGACTCCCCAGAAGGTATACCAGTGTTTTTCTGGCATTTGGG
CACCGTTCCCCCAAAACACGTGAAGCTCTTTTCCCGCGTCCCCATAATTTTGGACGCCAGGGGCACCCAAGCT
TAGCGCCCCTGTTTGGCTCCCCCACACCGCGAAGCCCTGCTCCCTGGGGTTCACGACAGTTTGGGACTTTATC
TGCCAAGTTCCACAAACTGATTGGCCCCAAGCTGGGGTCCCTAAATTGTACACAAAGAACCCCAGCCCCCCCC
CCCAACTCCAGTACAGGAAGCGATGGCCCCAGGGA
CCCTCGGAGTTGGAACGTGGCTTCCTAAGCCTTCACCAAAATTGAGGCTTTCCGCGCATGGCGCGCTGATGCC
CTTGCTGAATCAGAAGCACTCTGCCCTCTGATTCCTGCTTTCCACAACCCTGAGAGCATGATTTCTGGTCCCC
CAAACTCACTGAGCAAAAATCTTTTTGTGGGGGCTGCAAAGATAGGAGGCATTTCTCTCCGGACCTCTCCAAA
CTCCCTTGCCTATAATCAAGTTCCCTAAAACTTAGACAGAGCTTCCCAGGCCCCAGAGGCACACAGAGCCATT
ATTGGAGCTGCGTTTAATGATGACAGGGACCATGGGTCATGCAGCTCCCCCAAGTCACAAATGCCCCAGGTAT
CCTTCGCTCCAGCCAAGCCCAAAGCAAACTCTTGC
ACAGATCCCATATCTTGTTATGTCAAGCGCTTTGCCGTGTCCCAGTAAACAAATAGTCTGAGTGTTTTCTCCAC
CTCATAACATTCGGAATATTAAAAAATTCCCTGGGCCCCCGGAGCCTGACAGACAAGAATCCGGGCTTCCTAAA
ATTCAGAACTGATTCCCAAATCCCAGGGCCAACGCCAGACCCTCTCCCAATCTGGAGCCCCTCCGACTGGACAC
ACTGGACTCCTAAGTATTACGCGCTGTCCTCCAGGCGCACCCAAATGCATTCAAAGTGACGCTTTGGTCACAGA
AAGGCACTGATTTCTTGGGCTCCAAAGCAGCCCATGCACCCCCGAGTCACCCCAAACTTAGTCAGCATTTCCC
GGGTCTCCCTCCGCACTGCAAACTCCCAACTGCGG
ACACCGGTTCTTCAGGACCCACCGCCTAGACGGTCTTAATCCCTTTTCCCCCAGACCTAGATTC

Contig 8' (371 bp)
AGATTCAAAAACTATTTTTCTGGGGCCTCCAAATTGAGGTGCTGCCTGCCAGTCCTCCAAAATAAACTCAGGG
GTTTTTTGTTTGTTTGTTTTTTTGTTTGTTTGTTTTTTTTTTACCTTCCACGAAACAATCCAACTTTTTTGGA
CCATTGATTTATGGGTCCCCTGACTTTATGACCCTTGCCCCAAGTCCCCCTAAATGTAGGCCATTTTCCACGG
GCCTCCCAAAATGAAATTGCCCAGATCCCGCCGAAAAAAATATCCCCGGGTCCTGGAAATGCCAGGTATTACA
GGCCTGCGGCTGACACCCCTCCTTCCTACTAACCAGGTTCCCTGAAGTTTAGAGATCACTACCTAATGAACAA
ATCCAC

Contig 9 (2415 bp)
CCAAAACTGGGGCCCTATCTTACTAGGGTTCCCTAAATGCAGACAGCGCCCGGGAAAATAGGGGCGTTTTTTT
TCCTGTTTGCCAAAAATAAACTAATTGAAACCAATTTTTAGAATTAAAATCTAAAATGACCTTGATTTTCTGC
GTTCTCCAAATGTACTTTTCACAGCCCAGGTTGCCCCCAGTTTAGACGGTGTTGCTTGAATCTCTAAAGCACC
CTGAGGATTTTTCCCGAGGAAGCCACCACAACTACGGAATTTACTGTCCTTCGGGGCCCACAAGCCTCCAGGCC
ACCAACTTGGATTTCTAAACCGTGGAAATCAGCCTCCACTTCCCTCCGCCACCCCGAGGGGTCTGCTCAGACCC
CCCAAACGTGCCCGCTGTTCTTCTCCCCCCAAATT
TTATTTAGAGAATATGCCTCTCTCGGGTTCTGCCAAGTTTCCCGCTCAGACTTCCTCGGTCATCCCCAAATCC
TCTTCCCCACAGTCCGGGAGCCCCCACAAGCTTACCGACCCACATGCTGGGGTCCCCCAACTTAAACGCCATC
CCCTGTCCCCCAGATTCACCGAGTGATTTCCCTGGTCCTCAGACTGGGACTCTTTTACTGGAGTCTCGAATTT
AGCCATTAATCACAGTTCTCCACTCCGACGCAGGCTCCCTTGGGTCCCCACGTCGGGGACATGGGTTCTCTTG
CCTGCAAATCAGGCTGCTCTGACTTGCATTCAGGCCTTTGGGCATTGTTCCCCGCCCGCCGCGGTCTCGGTTC
TCCCCCCATCCCGCGCACGACGGGCACTGGGTCTG
GGCCTCTTGGTGTCTCCTACAAGTCCCCGGAGCTCCTCGGACTTGGGAACTGTCTCTTGCGTTCCCCAAATAC
ACTCGGCCCGGCAGTGTGTCCGCCAGGACGTAGGCAGAGCTTCTCCCGCGTCCAGGAAAACGACTGGGCATTG
CCCCAGTTTCCCCCAAATTTGGGCATTGTCCCTGGGTCTTCCAACGGACTGGGCGTTGCCCCCGGACACTGC
GGACTGCCCCCGGGGTCTCGCTCACCTTCAGCGCGTCCACCGCCCGCTGCAGAGCGCTCCCTCTCCGTCTCTC
GGCTCCCAGCGCGCTTGGGGACGCAGCCTCCGGGCCTCCAGCCTTGCGGTGAGCTCCCCGTCGCCTCGCGTGT
CCCGGCCCGGCTCCCAAACCCACTCGCGGCCGTCC
CGCTGGGGCTGGCACTGGCCTCCGGCGACTGCCGGGGACACGGGAGCGGAGCGCGGGAGCCTGCTGCAGGCCA
GCCCGTCGGCCGGGCCGCGCGCCCTGAAACGCGCGCGGCTTTCGTTTGCTCTTTGCAAAGGTCACAACCGTGG
GGAAAACGCCTCGGCGGCCCCCAAGCGGGGCAGGCAGGGCGTTGGGAAGGAGGGACACGCGGGAGAGGAGCAC
CCCGCTGGGGCGGCGCAGCGCGGCGCCCTCCAGCCGCCGGGCGGAGGATCCCGGGAGGCGCGCGCGGAGCGCGG
GCGAAGTGATTGATGGCGGAGCGAGGGGGCCAGCGGATCGCGGGGCTTCCGCCGGCGGCGGCCCCTTCCCCTCG
GAGGGACTCGGGCGGCCCGGGTTTCTGGGGGCGGG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
CGGGGCGCGGGGGCTTGTGCGTGGTCTCCACTTGGTAAAAATCACAACGACTTTTTACGTCGCCCCGACTCTC
CAGGAGATGGTTTCCCCAGACCCCCAAATTATCGTGGTGGCCCCCGGGGCTGAACCCGCGTCTACGCAAGGCC
AACGCGCTGAGGACGGGGGAACCATTATCCGGATATTTTGGGTGGGCCCCCAAAGCGAGCTGCTTAGACGCGC
CCCGGTGAGCTCGGTCCTGCAGGTAGGCTTGGAGCGAGGTTCCCCGCCCTGCTCCTCTTCTTCGGGCAGGCG
CGGCCAGGCCGGCCGGCCCTCCCCACGTACGGCACCTGGCGGCCGGCCGAGACGACTCCCCGGTTCCCGCGCGG
CACCGGGGGGCGCTCGGGCTCTGGCTGCGGCTCGA
GGCGCTGCGCCTGCTCGGGCAGGTGGAGGCTTCACGCCGGGCCCGCGCCCAGGGACGACCCCTTACCCCGCAG
GTCCCAGCGGGACTCGGGGCCCCCGGATCCAGCGTCTAGCCACCTGTGCCCGCACCGCCGCGAGGGCTTGTGA
CACCTACCACCCTGGCCGCCCCGCGTCCCCCCGCGCACGAATGTAGGGATCCTGACACCCCGGAACCTAAGAC
GGGGCCCCCATACACTTTCGTACAGCGATTCGGGATTTCTCTCGAACTCTGCAGATCTGTATGGCAAAGTTGA
TGGCCTGCATTATTTTTCTGATAATTCAGCGAAAGATGGCGACCAGAGCTATGCGCGTCTGGGTTTTAAAGGC
GAAACCCAAATTAACGATCTGGTCAACGAACAGAT
ACAGCATACGTTTTT
```

Contig 10 (3753 bp)

```
AGATTCCAATGGGGATCCCGATGAGGAAGCCGCTGCTCGTGCTGCTCGTCTTCTTGGCCTTGGCCTCGTGCTG
CTATGCTGCTTACCGCCCCAGTGAGACTCTGTGCGGCGGGGAGCTGGTGGACACCCTCCAGTTTGTCTGCGGG
GACCGCGGCTTCTACTTCAGTAAGTAGCTCAGCGGGGCACGGGGGCGGGGCGGACACAGCAGGTGCTCCATCG
GTGCTGCCCCGGTACCTGTGCCGGTCCTTCGGGATGGATGGTGTGGGGGACGGGGGGCGGGGGGCGGCCAAGG
GAGGACCTCTCCTCCGAGGGTCTGAGACTTCAGAGCGGGGGCGCCCTGGCCCTGCGCAGTGATTGGCACCTGC
CATGTGCCTGGCTGGGGCTCACACCCCCTGACGTTCCTGCAGCGTGACTCGAAACGGCAAACCGAAGGGACGG
GTGGCACGGGTGGGGAGGCAGACCGTGAGTGGCAGGCGTGCCGAGGGGTTCTTTCGGGCGGGGTGGCCCAGGC
AGGCCCCACAGGATGACAGCCTGTCCCCTCCTGCTCCTCCTTGACCTGCCCACAGCCAGGGCTGCAGGCACTG
ACATTCACCCATGGTATTGTGGTGCCTGACGTCTTGGCAGTGGGCATGGGTTCATGGACTGTTGGATTGAAAG
TGGAATAAGATGGGTTGAAAACCAATAAGAATAAAGGCGCGTGTGGCTGGCGGCATCTGCGAGAGGTGACCGC
TGCCCTCCCTCGGGGTTGGGCTTTGGGTCGGGTTCCCATGGGTGGGGCGGGCCGCCATGCAGGGTGCCCGCCTGC
TGGCCTCAGAGTGCTTTGCCGTCCTCATCTTTCTCTCTGGCCCCCGTCCCGCTCCTGAGGCTGGCTCGGCTGGG
CCCGCGGAGACCTCCGCTCCCGCCTCGTCTGTGCCCAGGGAGCAGGGTGGACCCTCCCTTCGGGCTCTTGCCTG
CACCTCCCAGCAGGCTGGGCCTCAGTGTCCTTACCTGTAGGATGGGTCAGGGGCGTCCTGGAGAGAGTCCTCG
GGACAATGGGGAGGCTGGGGGCAGGCCCAGCCTGACCCTGAAGGTGGGAGTGTGTGTCCCCCTGGGCTCAGC
CAGCCGCGCTTGGGGCCGGGAGGGGGTGGGGGACGTGGCTGGGGCAAGTTGTCAAGGGCCGCGGAGGCTCACCC
CCGCCCATCGCTCCCCATGTGGCAGCCTCTTCTGCAGCCTCTACTTACCCACCCTCTGAAATGGGCTGAAAAC
ACCCATCTTGGCATGCCAAAGCTTCTCTGTAAAAAGCGTTGCTGCTTCTTGATGCTTCTGAGGCCCCTGCCTG
CCCTGGCCTCTGAGCCCTCTCTCTCCTGCCTCGTTTGGGGGCAGGGAGTGGCACCATAGAATCTGGCGCTGGG
CCTGGGGAGCGGCCCCCTCGTGCCAGGCTTCCCCGAAAGGAGGGCTGGGCTGAGCTCCCGACCCTCTGGACCC
CTTACCAGGACCCCTTACCAGGGGCTTCCCCCCCCCCCCCCCGGTGGCGGCGGGCTGGGCTCGGGCCTTTT
CCTTGCAGCCGAGTCGGAGCTGTCGGAGGCGAGGGCGAGGACGGGAAGAGAGGAGGGCGTGGTTTCTGCTGGT
CCTCACTCCTCTCCTCCCGTCTTCCTCCTCCTCCTCCCATTCCCACCTGTGTCTCCGGGTCCCGGGGCCGCAG
GCTGCCCAGGCGCCTGCTGATCCATTGGGGACCGCCACTCGGGTCCCCGCTGGCCTTCGGGTCAGGGCCACGGC
CCACCTATTTTCCAAACAGCCTTGGGTCGAGGCCCAAGAGGCTGGGCCCGGTTAAGGACGGGGAGGGAGGCG
CCAAGAGGCCAGGGGCTGGTCCCGAGCACGCCCCGCACCCGCTCACCCCCGCTGTCCCCTCTCCTTCCCCGGGG
GGCCCCTGTGCACCCCACTCTCACTTCTTCTGCTCGAGGCCACGAGGCTGGCTGTCCCCGCAAGGTGACCGGG
CGTCCTGTCTGGAGGGCGGGGGCGCGGGGCGGCTGGGGGCACCGTCCGTGCCCGGGGCCCCTGTGCTGACGTGC
CCTCCCCTTGGTCCTGTGGGACTTCCAGGCAGGCCGGCAAGCCGCGTGAACCGCCGCAGCCGTGGCATCGTGG
AAGAGTGCTGCTTCCGTAGCTGCGACCTGGCCCTGCTGGAGACCTACTGCGCCCACCCCCGCCAAGTCCGAGAG
GGACGTGTCGACCCCTCCGACCGTGCTTCCGGTAAGGCAGCCCCTCTCTCGGCAGCGCCCCCCCCGGGGGGG
GGCTGTCTCCTCTGAGCCGGGGGACCGGGGCCCAGCCGGCTCTTGGGCTTCAAGTGCTGCCAGAGGGGCCTTC
CCCGCTGGGGACCCTGGCCAGAAGCCAGGGCAGTCTTCGCTCTGTCGCAGGGCAGGCAGGCAGGAGGACCCCG
CAGAGGTTGTTGTTCTGGGACAGGGGCTGGGGGGCCAGGCCCCCCCCTGACGGGCCCTTCCCCTCTCAGGACA
ACTTCCCCAGATACCCCGTGGGCAAGTTCTTCCGCTATGACACCTGGAAGCAGTCCGCCCAACGCCTGCGCAG
GGGCCTGCCGGCCCTCCTGCGCGCCCGCCGGGGTCGCACGCTCGCCAAGGAGCTGGAGGCGGTCAGAGAGGCC
AAGCGTCACCGACCCCTGACCGCCCGTCCCACCCGAGACCCCGCCGCCCACGGGGCGCCTCTCCCGAGGCGT
CCGGCCATCGGAAGTGAGCCAAATTGTCGTAATTCTGCGGTGCCACCATCCACCTCGTGACCTCCTCTCGACC
GGGACCGCTTCCATCAGGTCCCCCTTCTGAGATCTCTGTACCCTTCTGTCTGCGGGCATCTCCGCCCCGGGCC
CCGTGCCCCAACCTCCCCATGTCAGGCTAGTCTCTCCTCGGCCCCTTCCATCGGCCGAGGGCATCCAAACCA
CAAACCCAATTGGCTTGGTCTGTATCTCCCCCCAAATTATGCCCCCAATTATCCCCAAGTTACATACCAAAAA
TTGAACCCCTCAACCACACCCACATACAATCAGCCCCCGTAAAACGAATTGGCATCTTTAAAACACCAGAAAA
GCGAATTAGCTTTAAAAAAAAAATAAACCCAAAATATCAATTAGCTGAAAAAAAAATACTAAAAATAAATTG
GCTTAAAAACAATTGGCAAAATAAAAGAATTTGGCCCCCCCCTTCCTTCTCTTTCTTTTCGGACCTTGAGTTA
AATTGGCTGTGACCCATCATCCAAGAGAAAGGAAGGGACCAAAATTTGCAGGTAGGCTTGTCGCCGCTCACAG
CCATCTCCCTCCTCCTGCCACACCCTCGCCGGCCACTGGCGGTGTGGCACCAAGGACCCAGTCCCGTCCTCTC
TCTAGTCCCATGACCGAGACCGCGGTGGAGTTGGCTGGGAGACCCCGTGAGATCAGAGGAGGGGAGCACGGAA
CCAGAAACCCAAACCTGCACAGGTACAACATGACTGGCCCCCCGCACAGCCCAACACCTCTCATCTCAGTCTC
CACTTAAAAAGCACCTGTACCCACACGCATCCCTGCAGAAACACACACACACACACACACACACGCACGCA
CGCACACACGCGCGCACGCACGCGCACACACACACTCATGCGTATACACACACACACACGCACGCACGCGCAC
```

FIGURE 6, CONTD.

CCACACACACACATGCATTCACACACACACACACTCGTGCATACACACGTGCGCGCGCACACACACACACACA
CACACTCTCTCTCTCTGTGGGATCCCTGAG
Contig 19 (500 bp)
TGGCTCTGGCATAGGCTGGCAGCTGCAGCTCTGACTGGACCCCTTGCCTG
GGAACCTCCATATGCCGTGGAAGCGGCCCTAGAAAAGGCGAAAAAAAAAA
AAAAAAAAAAAACAACCAAACAAACAACAAAAAGCCAAAACACACAGAACTC
ACAGACACAAGAAGAGACTGGTGGTTGCCAAAGGTGGGGTCGAGGGTGGG
AAAAATGAGGAGAGGGGGCAAAACACACAAACGTGCAGCCATAAAATGGT
AAAGTCCCGGGGACCTCCGGTAGCGCGTGTGGGGACTCGGGTTGAGAACA
CACCGTGATGTGTATTCGCGAGTTGCTAAGAGTCCCTGTTGGAGAAACAA
ATGCGTATCGACGTGTGGAAATGAAAGTTAACCCGACCTGCTGTCCTGAT
CACTTTGCAACACATACAGACATAGAATCATTATGTTTTACCCCTGGAGC
TGACAGCGTTATACGTCCCCCAGCCTCAATTTAAAAACAGCGTTGCCGTG
Contig 20 (400 bp)
TTCATACTGTGCAATGCCAGCCTTAAATGCACAGAGGAGAGCATTAACTT
CTTTGCAGAATCACTGAAATGATACCACTCATGTTTTGCAACTTGCACTT
GGGCGTTATTTTATTGGTGCCGGAACAGCGCCGATGTGGCACCAAACTAG
CGCCGCTGTTTTTATTTCCCCTCGGTATCCGCGCTCTCGCTGTCTTCCCC
CCCTTCCGCTTGCAGCTGAGGAAAGGGCTGAGAGGAGGAAAGTCTGCATT
CACCCATCTCCCCCTGCCTCTGTTGTCATCCTTCACAGAAGTGGTGGCCT
GTGCGGGGAAGTCACTAAAACCTAGGCAGGTGTCCCGTGGGGTCATGCTTG
TTACACCTTTGTGCACCTGGCCCAAGTTCTCGGTGGAGCGAGAACGTGGC
Contig 21 (559 bp)
AGCTAGCCCCCCCAGCCAGGGCCAGGCCTCTCCTGCCCACCCGCCCAGCCA
GCATGTCTCAAGAGGAGGGGGCCTCTAAGGGATGAGGACCTGCTCCAGTC
GGAGACACGAAGCCCCGCCGGCTCCTCCCCGAAAGTCCAGCTGCGGCTTT
CGAGCACGGCTGCGCCCTTCGTCAATCATTTCAGCCACAGAAGTGAAAGG
CGCTTTCGTGGCCGAGGCAGGCGGGACACAGAATGGAATCCCACCCCAGA
GCGAAGAGCCGCCGTGGGTGAAGCGCGTCTCTGGTGGGGACCGGGCCGGG
AACTTCACATGGGGGTCGCTGTCCCCATCTCCCCATCGTCATTACTGCAG
GGGCTCGGCCACACCCGGAGCTGCGGGGGCCAGTGCTGGACACTGGACCT
GGCCTCCGTCCTATGATGTCATGGGGGCGGGGCCAGCACAGGGCAGTGGC
CACACCTCGGGCCTCCCAGCACCAGCCAGGATGGCAGAGGGCCCCACCCC
ACCACGGGGCATGTACATCCCAGAGGACCAGCTGAGCAAGGCTTGATANG
GGCTTCAAC
Contig 22 (450 bp)
CGTGCAGGGACCCGTGCGGGGCCTTCCTGTGGCCACAGAGAACAAACACAC
CATTATCTTCAGCCCCACCGCGCGGCCTGTTAATGGGTAAACTGGGGCAA
GGGGGCCCCTGCCTGAGGCCGGGGTGGGGAGCGCAAGGCATGGCCTGTGT
GCCCCAGCCCAGTCCTTCAGGGCGCTGCTGTCCTGCACCGGGGCCCCCAG
GAAGCAGAGCACCCAGCTTCTCCCCTATTCTAGAACCAGCCCCCAGAACC
CTGGACCCAGACCCAGGCCCAGGGGATACTGACAGAGCCACGGCAAGGCG
GCCACTCCACACCCCACAGAGGGGCCAGCAAACCCCAGTCACTGCGCAGC
CCATGCCCAGGGGGCAGATGGGACACGAGAGCAGCCCTCATCCACAGCAG
GCAGGGGAGTGAACTGGTGCAAAACGGGGCGGTTCCACGAAAGTTAAGCA
Contig 23 (535 bp)
TGCCAGAGACCTCAGAGCTGGGCTCTGCCTTCCCGGGCTGACACGGAGGG
CTGTGGCTTCCACCACCCCAGGCCACAGCCAGCCTGCCCAAGTCCCTGAA
GTGTCCCCAGAGGTGGCCCTGCCTCCACGCCCAACATCAGGCCTGCTGCA
GCCCTGGACGGCCCCCTGTCCCCCGGAAGCCCTCGGGGCTCTCTCGCGTC
GCCTCTGGGGAACCCTCGGTAATGTGGCCCAGCCGTGCAGTGGCCGGATC
ATTTGCTCAGGGGGGCCCAAGGCAGGGGGGTGACACATCCGCAAGTACCG
CATATGCACAGGATATGGATTGGGTGTGGATTTAACCTTTTCGCAAATGT
CTCTGCCGGTACAAATATTGTTTCTAATCCTCTGCCTCCCTGAGCCGGTG
AGTCTGCCCGGGAGCTGCGGGGAGCTGGCTTGCTGAACCTGCCCTGGCCC
CCACCCCCAAGGGAGCCCCCGGCCAGTGCTGAGGGCAGGAAGCTTGGGCA
CAGGCTGCAGAGGCCAGCGGCTGGCCTCAGTCACCT
Contig 24 (868 bp)
TATTGAAGACCCTATCATGAGTTCCCAGAGCGGAGGGGTGGAAGCAGGGG
CCTACAGCCCACTCCCCATCACTCCAGACCCGTCCGGGGCTGGTGTCCCC
TGCCCCCTACTCCTGTCTCTGGTGGGCGGACGCTCGAAGGAGGCACTCTG
GCCTGGAGCCTGGAGGGTCCCTGAACTCCCGCTGCCACCTGGGCCCTCGG
GCTCCTCCTGCGCTGGGACCCGCCGGTGGTGGGAAGCAGCCCTGCTCAGTG
GGAGGAGGCAGGGCTGTGGCCGCCCCGCACGGCCCTGGGGGGGACGCACG

FIGURE 6, CONTD.

```
CAGGACGCANGTGGGCGTGTGTGAGTCCGTCTACACGTCCAGCCAAGGGC
GGCCGCGACCGGCCAGGGTGGGCAGCCCCAGCCTCAGCAGGGCGCTCTCT
GGGGCTCAGGCTGCGCCGACGGGAGATGAGGGGTGAGGCGCAGTCTGGGG
CTGCTGCCGCAGAACCTCGCCCAGCTGGCAGCTGGGCACAGGGAGACCTG
TACTCCCAGAACCTGAGGCTGGACGTCCGAGACCCGCGTGCCGGCCTCTT
GGGTGCCTGGTCAGGGTCCTCTTTCTGGTTTGTGGGCAGAACCTCCTCAG
CGCGTCCTTGCATGGGGTGCTAATCACGGAGTAAGGAGCCAGAGAATGAG
GCACGGAGTATCCAGTGTTAACCCTGGAGTATGGAGACGGGAGTACTAAT
TGTGGAGCATGGCTCTAAGGAATGGAGTATTCGTCACGGAGAACGCGGGG
CCGGGTGAAATACGGAGAGCGGCGTACGGACAACGGGGACGGGGTATCCG
AAGGGGGAGGATGGAGTATCGGCCGGAGGGTGGAGAATGGACACTAGAGGA
TGTATANNGGGCGTCAAT
```
Contig 25 (500 bp)
```
ACCAGTTTCGATGAGCAATCCCAGCGGCGTAACATTATGGCTGCAGCCTG
GTCAATGCCGGTGGAGTTTGAACCTCCACGCGTGGCGATTCTGGTAGATA
AATCGACATGGACCAGGGAGTTGATTGAACATAACGGTAAATTTGGCATC
GTTATCCCGGGCGTTGCAGCAACTAACTGGACGTGGGCGGTGGGAAGTGT
GTCGGGGCGTGATGAAGATAAATTTAATTGCTATGGCATTCCGGTTGTGA
GAGGCCCGGTATTTGGTTTGCCTCTGGTCGAGGAAAAATGTCTGGCGTGG
ATGGAGTGTCGATTGCTACCTGCGACTTCTGCGCAAGAAGAATACGACAC
GCTGTTTGGCGAAGTAGTATCAGCAGCGGCAGACGCACGGGTATTTGTCG
AAGGCCGCTGGCAGTTTGATGATGATAAGCTCAATACGTTGCATCATTTA
GGTGCTGGGACGTTTCTTACCAGCCGCAACCGTGTTACGGCGGGGTTAAGC
```
Contig 26 (500 bp)
```
ATGTTTGATGTCCGGCGCGTGCTGTAAAAATTTACGCTGCTCGCGTTCTTT
GGCTTCGTCCACCACCGGAAAACGGACAAAAATTTCCGTCATACCTTTTT
CTTTCAGGCGGAAGCCAATGTCGTAATCTTCAGTAAGACTCTGCACGTCG
AAAGCAATACCGTCACCGTCAGCTAACAGTGCGGTCACGGCGCGGCGGCT
GAAACAGGTGCCGACGCCTGGCGTGGGCACTTGTCCGGCGAGGGCTTCAC
GCACCGGAACATCTTTGCCATGCAGCTCTGAAAACTCATCAATGTAAGTC
ATGCTCGTGAAGTGCGTCCATTCGCGTTCGAACGGATACACCGGGATCTG
AATCAGATCTTTACGCTCGACCAGATAGTTGAACAGACGCAATTCCATCG
GTGAAATCACATCTTCGGCGTCATGCAGAATAAAAACCACCAAAAGCGAAA
TTGGCGCTACGCTCAAATTGGGTGATGGCGTCCAGCACGTTGTTCAGACA
GTCGGCTTTGCTGGTGGGGCCAGGACGCGCGCAGACTACCTTATGCACAT
TCGGGAAGCGAGCGCACACTTCGTCAACATCACGCTGAGTATCGGGGTCG
TTGGGGTAGGTGCCAACAAAGATATGATAGTTTTCGTAGTCGAGCGTGGT
CGCCGCCAGCTCGGCCATATTGCCGATGACGCCCGTTTCATTCCACGCCG
GAACCATAATCGCTAACGGTTTTTCATCTGGTTTATACAGTTCGCGGGTAA
CTCATTCGCGGGTAGCGGCGATAAACACTCAACTTGCGTTTAATGCGGCG
TACCCAGTATACGACATCTATAAAAAAATCGTCCAGCCCGCTGATGAACA
TGATGACCGCTAACGTTATCGCGATTACTTTTAAGCCGTATAGCCAGGTA
```
Contig 27 (500 bp)
```
AGCTGGATGCCCCCAGCTGTGGTCCCTTCCCTTCCCTCAGGGCAGGTTCT
GTCCCTCTTGCAGCCACCGTCACTGCTGTGGACAGGTCTGCACACCCGCC
GTCCACCAAGAGCGTGGCAGGTCCCTGGGCACGGGCCGGCTCCTGACGCA
CCATGTGTTCAAGGCAAGAGCACTGGACAGAGGGTCCAGACGTCCCCTTG
TCCTGCTCAGGCCTGGGCGGGGGCAGCCCTGGCGGGAGAGGCCCTGGGCA
TCAGAGCCTCTGTGGCCTGGAGCTTGGCGCCCTGCCCTCCCCACCTCCGT
CCTGCTCCTCGCCGCGCTGCACGGACCTCTCCCGGCCCCCCAGGCTCATT
ACTCTTAAGGACCCTAGCCCCCTATGCTGAAATGCTGTACCTCGTGCTTG
TTTTCATCTGTTTATTACCTTATCTTCATTCCTGCTTGATGATATCTGGT
TATTCTTTATTGATTATATATATCTTGTTCGTGTTTTTATAGGACACTGT
```
Contig 28 (450 bp)
```
AGTGCGGTCGGGCCGTCCTGACGCTCAACACCGTATTTCCACGCGACCGC
GGATTCAACCTGGTCACACGGGACGCCATGTAGACATGTTCGGGGTTACGC
GCAGAGAAGCGACCTGCTCAACCGGCTGGTGAGTCGGGCCGTCTTCGCCC
AGACCGATGGAGTCGTGGGTGTAAACCATCACCTGACGCTGTTTCATCAG
CGCAGCCATACGTACGGCGTTACGTGCGTATTCCACGAACATCAGGAAGG
TGGAGGTGTACGGCAGGAAGCCACCGTGCAGGGAGATACCGTTAGCAATC
GCGGTCATACCGAACTCGCGAACACCGTAGTGGATGTAGTTACCCGCAGC
ATCTTCGTTGATTGCTTTAGAACCAGACCACAGGGTCAGGTTAGACGGCG
CCGGGTCAGCAGAACCGCCGAGGAATTCCGGCAACAGCCGGACGAACGCT
```
Contig 29 (450 bp)
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCAGGCCAATCTGTCTGGTCTCCAATGGGGACAATTTGGTTCTTTAGGCT
TCTGTCCAATGGTCCGAATGGCCCACTCCCCGGGCGCCGGCCAAGGGTCC
TCTGTGCCTCGGGTGGGCTGGCACGGACCGCCCCCAGGGTCGTGCCAGCC
CCGTCACCGGGGCCCAGAAGCTTCGGGCCTCTAGCTGGCTAGTCGGGCTG
CTGTGCAGGGGGGCTGCGCTGGGGGCAGAGGCGGGGGTGAGGTAAACCTC
CCAGCCGCCCGGGGTCCCTGCCGCAGCCCTAGGCGCCGAGACGGTGGCTG
GGTCGGTACCGCCAGACCCGAGGGCCTCGGGGCCCGGGTGACCCCAGCTG
TCGCACACGCTCGCAGCTCTCTTGCTCATCAGGGCTCATCCCTCTGGACC
TCTCCTACTGCCCCACCTCACCCCGCCTGGACCCCATGAAGCCCCGCGGA
Contig 30 (600 bp)
TAAAACTAGCTCTAGTAGAAACATTTTATTTAAAAATAAAAAACCTGACT
ACGTCGGGAGTTCCCGTTGTGGCTCAGTGGTTGACGAATCCGATGAGGAA
CCATGAGGTTGCGAGTTCGATCCCTGGCCTCGCTCCGTGGGTTGAGGATC
CGGCGTTGCCGTGCGCTGTGGTGTAGGTTGCAGATGAGGCTCGGATCCTG
CGTGGCTGTGGCTCGGGTGTAGGCCGGCGGCTACAGCTCTGATGAGACCC
CTAGCCTGGGAACCTCCACATGCCCTGGGAGTGGCCCTAGAAAAAGGGCA
AAAGACAAAAAAACAAAAGAAAAAGGAAAATAAAATAAAAAAGACTATGT
AAATGAAATTAACGACTGCCTAGGGTGGGATTTACAGCATGGGAAGTACA
GCATGGCCGTGACAGTGCAAGGGTGAGGCGGGAAAATGGAAATAGGTTAG
GTGAGTTTCTCCTGCTATTTGTGATGTGGTCTGCTATCGCTTGAAGACGG
ACTGCAGTGAGATAAATATGTACAGTAAGCATCCGAAAAACCGCCAGAAC
GGCAAAACGAATGACTCCAAGTAAGAACCCAAAAGAGAAAAGGAAATAAT
Contig 31 (450 bp)
GCGCGGGCGTTCCGGCTGGGGTATTTAACGTGGTCACCGGTTCGGCGGGC
GCGGTCGGTAACGAACTGACCAGTAACCCGCTGGTGCGCAAACTGTCGTT
TACCGGTTCGACCGAAATTGGCCGCCAGTTAATGGAACAGTGCGCGAAAG
ACATCAAGAAAGTGTCGCTGGAGCTGGGCGGTAACGCGCCGTTTATCGTC
TTTGACGATGCCGACCTCGACAAAGCCGTGGAAGGCGGCGCTGGCCTCGAA
ATTCCGCAACGCCGGGCAAACCTGCCTCTGCGCCAACCGCCTGTATGTGC
AGGACGGCGTGTATGACCGTTTTGCCGAAAAATTGCAGCAGGCAATGAGC
AAACTGCACATCGGCGACGGGCTGGATAACGGCGTCACCATCGGGCCGCT
GATCGATGAAAAATCGGTATCAAAAGTGGAAGAGCATATTGCCGATGCGC
Contig 32 (450 bp)
GGTGGATGCTGGCGATAGCGTCATCCTCGCTTATGCCGTGCAGCGGGCAA
GGATAAAGCGCGCGATAAACATGACCCGGCATCAGCCCCATGCCCGCAGA
GTACGGATTCACCTTGCCCGGTCAGCGCCAGCGTGTAATGCGTGCGCCCGT
GATACGCGCCGCTAAAAGCGATGGTGCCGCTACGTTTGGTGGCGGCGCGG
GCGATTTTTACCGCGTTTTCCACCGCTTCGGAACCGGTCGTAACCAGCAG
CGTTTTCTTGGCGAAATCGCCCGGCACCTTCTGATTCATAATCTCGCACA
GCTCCAGATACGGCTCGTAAGCCAGCACCTGGAAGCAGGTGTGCGACAGT
TTTTTCAACTGCGCTTCCACCGCGGCCACCACCTTCGGATGCAAGTGCCC
GGTATTGAGCACCGTAATCCCGCCCGCGAAATCAAGATACTCACGGCCTT
Contig 33 (500 bp)
ACGTGAGGTTTGGGGGAGGAAAGCGGGGGACGAGCAGCCCGAGAGGAGTG
GGGGCTGGCCTGTGGCTGATGAAACTCTGAGAAGGTTAAGAGCCCCCATT
TTTGTCTTCCTCTTTTTTTATTATGGAAAATTCCAAATGGATGCAAAAGTC
CCAAACCTAACTGGACATCTTCTTGGTACCAGGAACGGTCAGGCACTTAT
GATGCACCGAGCCCCGAGGGAAAAACCCTGCCGTCCTGGAGCCCACGGTC
CAGCAGGGCACACAGGCCCCAGCCCGCAAGCGGCACGGCTGAGTCAGTGA
ATGGCGTGCCCTCTGGTCAAGGACGGGCACTCTGGACCCCAGGGAAGCCT
CTGAGGAGCCCCCTTCACAGCGTCAAAAACTGTTAACAGGGCCATGTTCG
CACCCCCCCACACACGTGGTTCAGAAGCAGACCCCAGGCATCGTAATATG
TCATCCGTGAGTTCCCTGTGTGCCACCAACAGAAAGCCCATCGTCACGTT
Contig 34 (400 bp)
CGGCATCGATGTACATGGTACGCAAGGCACTCGTAAGGCCCCGAGCCTCT
AGGCCTTGTCATTGTCACGTGCTGCTCGCGGGGATCAGCAGCCAGGCTTG
TGACCCCGGCCACTTTGACAGATAAGGACACAGAGAGGCCACAGCACTGG
TGTGAGGCCCCACAGCCAGCAGCCCAGGGCAGGGAGGACTGGGTCTCACC
TGCCTCAGCTGGGCCCAGCCTCCCTGGGAGTCCCGGAGTCTCCCCAGCTT
AGGAGTGTCCCTGGAACCCTCTTCTCTCCCCTTCCCGCCCTCACCCGGAC
CCCCTGCCTCCCCCCCACCAACCCCCTCCCCCTCCTTCTTTCACCTTGAG
CTCCCCTCTGAGGACCTCTACTGTTCCTCCTTATCCTCCCCTTTGAGCCA
Contig 35 (500 bp)
TGGCGGTGAACTATGTCGTGCGTGAAGAGCATTTGTGGTCGGTAGCGCGT

**SUBSTITUTE SHEET (RULE 26)**

FIGURE 6, CONTD.

TATATGCGGGAAGTTTAGGCGAACTGGACAGCCTGGGTTTATCCGGTAGC
GAAATCCGCTTTCACGGTAAAACGCTGCTAGCGCTGGTGGAAAAAGCGCA
CACATTGCCGGAAGATGCCTTACCGCAGCCGATGCTTAACCTGATGGACA
TGCCGGGTTATCGTAAAGCGTTTAAAGCGATTAAGTCGCTGATTACTGAC
GTGAGCGAAACGCATAAGATCAGCGCCGAATTGCTGGCATCGCGTCGGCA
AATCAACCAACTGCTGAACTGGCACTGGAAACTGAAACCGCAGAACAATT
TGCCGGAGCTGATTTCCGAGCTGGCGTGGTGAGCTGATGGCGGAAGCATT
ACACAATTTATTGCAGGAATATCCGCAGTAAAATCTTCCGAAGCCGGACT
GGGCGCGCTCAGCGCCCACATCCGGCTTCGGCAAACTACAAATCCAACACC
Contig 36 (500 bp)
GATTTCACAAGCCTGACCCACGCGGAAATGCGCTAACAGCGTAAAGTCGT
GCGGCCAGAATTTTTTCGTCTCTTCGCTTTGCGTCAATTCAAAAGTCAGC
GCTACGCCATCAGCATCTTCATGATGTGATTTCAGCGTCCACGGCAGGTT
GCGGGCAAAACCGTGCGCAGGCAGACCTTGTTGTGCCGCCGGACCAAACC
ACGGCCAGCAAACCGGTACGCCACCGCGAATAGCGACGCCATTTTTGAAC
GGTGTGTTGTTGCTCAACCACAGAACTTCTTCTTCACCCGCAGGTTTCCA
CGAGAGAAGGTGTGCGCCCTGTAATGCAAAAGAGGCTTTTACCTGGGGAT
GATCGACCACAATGAGGTCCAGTTCATCCAGTTTACGACGGGAGAGGACA
GGGGAGATTTGTTCGATGACCGGAAGGGCAAAAATTTTCTTAATCATGAC
GCAGTCCTTTAACTTCATTTTATCAGGTAAAAAAAAGAGCGACCGAAGTC
Contig 37 (300 bp)
ACCTGATCAGGCTCTGCACTGTGTTCATCAGCGGAGCCGAGATATTTGAC
CGCCCCATGCATAACGGAAAGGCGTGGGTAAACCCCCGGGCGCGTTCCTT
TATCAAGATGACGTTCGAATATTCCGGCAGGTGCAGTTTGTTTATTCCAG
AAAGGCGTTGAGCGCGTATGAATATAATTCTGTGGGATTTGAAGCATCCT
TTTCCCTCCTTCGGTGAATGCGCTGAAAACGGCTTATTCCAGCCGGTTCA
GGGTACGCCTGATAATTTGCATTTTAAATACCATTTATTGGGTACTTTTT
Contig 38 (450 bp)
ATCCTTTTGGGGTCTGGCAATTACGCAATAAAGAAGGCCCCCATGCGATT
AAAGTCACCGGCCCACTGTCGTCTAATCATGGAGAAATTGTCCATCAGTG
GGGTCTCGATGGGCAGGGGATTGCTCTGCGTTCCTGGTGGGATGTTAGCG
AAAACATTGCCAGTGGTCATTTAGTGCAAGTGCTACCGGAATATTACCAG
CCAGCGAACGTCTGGTCCGTTTATGTTTCAAGGCTGGCGACGTCAGCGAA
AGTGCGGATAACGGTAGAGTTTTTACGCCAGTATTTTGCCGAGCACTACC
GGAATGTTTCACTGTTGCATGCCTGATTTATGATTCAATTATCGGGTTGA
TATCAGTTTAAAACCTGATTTTCTCCTTTCTAAGCCGCTACAGATTTGGT
AGCATATTCACCTTTAATCGCGCATGATCTAAAGATAATTGAAGAGGTTA
Contig 39 (450 bp)
AATGTACTGGCAAAAAGCCAATGGCGAAGCGTGGGGAACGTTACATGCTC
TGCTGGCGGATATTAATAGTCAGGGTCAGGTGCAGATGGCGATGAACGCC
GGCATCTATGATGAAAGCTATGCGCGCGCTCGCGTTTGTACATCGAAAACGG
TCAGCAGAAGGTGGCGTTAAATCTCGCTTCAGGTGAAGGGAATTTCTTTA
TCCGTCCTGGCGGCGTGTTTTATGTCGCGGGAGATAAAGTCGGCATCGTT
CGTCTGGATGCCTTCAAAACCAGTAAAGAGATTCAGTTTGCGGTGCAGTC
AGGGGCCAATGTTGATGGAAAACGGTGTAATTAATCCGCGTATTCATCCCA
ACGTCGCCTCAAGCAAAATTCGTAACGGTGGTTGGGATTAATAAACATGG
GAACGCCGTGTTTTTGTTGAGCCAGCAGGCAACAAATTTTTATGATTTTG
Contig 40 (400 bp)
GACATTAATCATTTCAAAATCAAAGCCCCGGTTTTCCATCGCCCGTTTGG
TGGCGTGGCACTGAACGCAATCGTTACGAGTGTAAATAGTAATGCGCATG
ATTCGTATTTCCGTTTAAAATGAAGATACGGCGCGATGATACGCGTCGGG
TTGTCTCTCTGTTGATACAGAGATACTAGATGTAGTTGAAAAAAGATTCA
ACCACACAATATATAGCCCAGTAGGGGTCGAAATTACCCTGGATATGAGC
GTGACGGGGTAGGGGGATTTTTGTGATTCACCAGCCAAAAAGAAACCCCG
AAGACAGGCTTCGGGGTCAAAGACGCGTATTTATTATCATTTTTGCACTA
CGATTTGCGCATGCTTAACAGTGCGCCGATTAAAATATCTACCGCAGCTG
Contig 41 (500 bp)
GCAAAATCACGTCCGCGACCTGGCGTTGTCGCTGGGCCATATTGGCAAAG
GAGCTGGATTGCGGTGCCTGCAAAGTGCCCTGAATAATGCCATTGTCCTG
TACCGGGAAGAAACCTTTCGGAATGAACACCCACAGCAGCACGCTAAGCA
GCAGCGTGCTGAGTGCCACGCTTAAGGTCAGCCACGGATGATTCAGCACT
TTCGCCAGTCCACGACCATAGGCGGCGATTATCCTGTCGAACATTTTTTC
CGAGGCACGGGAGAAGCGGTTCTGTTTACGCAACGACTCCTGGCTGAGCA
TCCGCGCGCACATCATCGGTGTCAGGGTCAGCGACACCACCGCTGAGATC

**SUBSTITUTE SHEET (RULE 26)**

FIGURE 6, CONTD.

```
AAAATCGCTACCGCCAGGGTAATAGCAAATTCGCGGAACAGTCGCCCGAC
GATATCGCCCATAAACAGCAGTGGGATCAACACCGCAATCAGTGAGAAGG
TCAGCGAGATAATGGTAAAGCCGATTTCACCTGCGCCCTTGAGCGCCGCC
Contig 42 (400 bp)
AGCTATCTACGGCAAAAGGCACGGTAGTCAATTTCGTTGTTAAATACATC
AAGCGTTTGGCGCCGAAATACCATCTGCCAGATGCCATTTCATTTCGTAG
CGCACTGCATAACGGCTACCGGATGCAGTACGTCAAACCCGAACTGGGGC
CGGAAGGATTTAGCTTTTCTGCAATACACCGGCGGCACCACTGGTGTGGC
GAAAGGCGCGATGCTGACTCACCGCAATATGCTGGCGAACCTGGAACAGG
TTAACGCGACCTATGGTCCGCTGTTGCATCCGGGCAAAGAGCTGGTGGTG
ACGGCGCTGCCGCTGTATCACATTTTTGCCCTGACCATTAACTGCCTGCT
GTTTATCGAACTGGGTGGGCAGAACCTGCTTATCACTAACCCGCGCGATA
Contig 43 (450 bp)
GATTAGCGCCAGATGCTCGCCATCGAAAAGTTGAATCAACCCCAGCTGCG
GGTAATAAGTGCGCGTACGAACAAATTCAGTATCCAGGGCTATCGCCGGA
AAGGCACGGACGGCTTCACACAAAGAAGCCAGCGCATCGTCCGTGGTAAT
CATTTGGTAATTCAAATTGTTTTCTCTTTAGTGGGCGTCAAAAAAAAACGC
CGGATTAACCGGCGTCTGACGACTGACTTAACGCTCAGGCTTTATTGTCC
ACTTTGCCGCGCGCTTCGTCACGTAATTCTCGTCGCAAAATTTTTCCGAC
GTTAGATTTCGGTAACTCATCACGAAACTCCACCAGCTTCGGTACTTTGT
ATCCCGTGAGCTGACGGCGGCAAAAAGTCACCAGTGACTCTTCGGTAAGC
GATGGATCTTTTTTCACTACGAAGATTTTCACCGCTTCACCACTCGAGCC
Contig 44 (750 bp)
GAGCAGCCCCGCGTGATGACAGGCATGCGCCCGCGTCGGCTCTCTCTCTCT
GGTGCACTGAGTCACAGGATGGCGGCGGTGGCCGCGGTGGTGGAAGCGGT
CCTGGAGGGCTCGGGAGGGAGGATGCGCTCAAGCTGGCTCCCCGTGGGGC
TGGCCCGGAGTAGCCTCCGTGAGGGCACCGTGTCTGCTCCCAGAGCCCGC
TCCCCGGCCTGCCCTGCCTCCCTTCCCTGCCCCAGTTCCCCCGGAGCCCC
TGGATCCCGATGGGAGGCGCCCCTGGGGAGAGGGGACCAGGGAGGGGCCC
AGAGCTCTGAGGCCACCAGACCTGCCCAGGACCCTTCGTGGGAAGAAGAG
GTGGGCCCCAAAGGCACCTAGAGAGAGGGAGGCTCTGCTGGCTGGGGGGC
CTTCCAGGCGGGGCTTCCAGGCAGGGCCAGTGTCCTGGGGGCTGGAGGGA
GTCCCTCGCTGCTGGGGGGGCGGCAGCAGCACCTGGGGCGTCTGGGAAGAG
AGCGGGAGGAGACTGGAGCCAACTGGGGGGGACACAGGAGGGGTCCAACCC
CAGCGGTGGTGTTGGGGGTGCTGGTGGTGGAGGCCCTGAGAGGCTGTGCT
GGGGGGGCAGAGCGGGTGCTGGGAGGGGCAGAAGGGGTCCCCAGGGCTCATG
GGCCCTTCGCAGCAGTGGCAGTTGGGGTGGGTGGCTGTCTCTAGGGCTGT
ACCACGGTGGGTGCCTGGAGAAAGAGGTCCTACCCCTAGTCTTTGCTGCA
Contig 45 (300 bp)
TGGGGGACCCCACTCCAGCCCCACTGAGTGACGCGCCCCCCTGTGGTCCCA
CCGCCAACCCTGCCTCACACCAGAGGGGCTGTGGCCACACCTTGTCCACA
GCCTGTCCCTGAGACCACGAGCCCCCGGGCTCAGCCCCCTCCTCACCCCT
GGACCGAGGAGAAGCCCCCACCTGGGCTCAGCTCTTGGAGCTAAACTTCC
AGGAAGGTTCTGGTGCCCTCGGGTCTTAGAGCATGGTGGGGAGGGGGATG
CTGGTGGGGGCGCAAGCCCTCCCCACATTTCGCACTCGACCCGGTGGGNG
Contig 46 (300 bp)
CCGGCTAGAAGCCACGAGAGCCCCCAGGCCCCGCCCGACGTCTCTCCTGC
AGGGATTCGGCAGCCCTGGGGCCACAGGGCCTGAGCAGACCTTGGGGTTC
CGGTGTGACTCCAGCCAGGGTCCCTACTGTGTAGGCACCAGGGCAGAGTC
AGCCCTGGGACCATGGCCACAGCTGCTCCCGCCTGAGCCGGGCCCCCCGC
CCAGGCTGGGCCCCCTCAGTGCACTGTCCCAAGCCAGCTGCTCTCCCCAC
CTCCACCTTCTCCATCCAGGTCCTGCCCCACGGCCTTTGCTCAGGCCCAG
Contig 47 (500 bp)
TTGACTGGCACTAGCACGAGCTCTGTACCCGGGGATCTGGGCTCGGGAGA
AGGGAGACCCCCCACCCGGCAGGCCGAGGGCGCTGTCACACCATGACTCT
CAGCCTTCCCCACCCGACGGACAAGAGTGACCCTCTCCCAAGCCCCCACT
CACCCAGGACCGCACACCCCGTGAGTCCTGCGAGTGGGGGCGGCTCAGGG
GCCCCGAGTCCCAAAGGAGTCTGCTGGCCCTGGGGGGGAGGGGAAGCAGC
AGGGTGGTCACGGGTCTCCCTGGTTGGCAGGACCACAAGCTCAGCCCGCT
GCCTCCCAGAGGGCAGCGGACACCAACCAGTCCGGGGACCCCACGTACC
TCAGCTGCTGCAGGTGCCCCTGCCTGTACTGGTGCCAATGGGGCCGCTGG
CTGCTCCCATGGACAGCTCGCCACTCATCCCAGCCGCCTACCCCCCTTCC
GGGTCCAGTGTCCGGCCGGCCACCCGCCTGCCCAGCCCTGGCCTCCTCTC
Contig 48 (500 bp)
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
GGGGTTGCCGCAGGCTGCTGTGTAGGTCGCAGACGCAGCTTGGATCTGGC
GTGGCTGTGGCTGTGGCTGTGGCTGTGGCATAGGTCAGCCACTGCGACTC
CGATTTGACCCCCAGCCCGGCAACTCCCACATGGCACAGGTGCAGCAGGG
AAAATAAATAAATGAAATAAAAATAGGTGAAGACAGTGGATTTCATCTCT
TGGGGTTGCGGTAAGCTCTACACAATAGGGAGTTTACCATTTTACCTGTT
TCAAGTGGCACTGAGTCAGCTCACAGTCCTGAGGGCCCACAGATGCCGTC
TGCCTGGGAGATTGTTCCTCTCACCACACTGCCCCTCTGTCCCCACTAAA
TACTCACTGCCCTCCCCGTCCCAAGGGCCCCTGCCCCACCCTCTGCTTCC
TGTCTCTGAACTTGCTGGCCACCAGCGACCGTCTGGTGACCTCACTCTTC
GGCCCCATTTGTCGCACACCCCACCTGGCCTCTCCCCGGCATGGGCAGAN
Contig 49 (600 bp)
GGGATATTTGGGGGCATATTTGGGGGGGAGATCCCCACAAGGCATTTGGG
GTTTGTGGTTTGGAATGCCCCCGGGCCCGATGGAGGGGGCCGGGGAAGAA
TCTAAGCCTTACTTGGGGAGGGTTGGGCCCCGGGGCCCCGGGGCCGGAAAT
GCCCCCAAGACAGAAGGTGTACAAAATTTCTCAAAAGGGTGACCCTTAAT
GAAACGGGTCCCGGTTGGAAAGAGGTCACCAGGGTGGATTGGTGGCACCG
CAGAATTTACGACATTTTGGCTCTCTTCCAATGGCCGGACGCCTGGGGAT
AGGCGCCCCCGTGGACGGCGGGGGTCTCGGGTGGGACGGGCGGTCAGGGGT
CGGTGACGCTTGGCCTCTCTGACCGCCTCCAGCTCCTTGGCGAGCGTGCG
AGCGCGGCGGGCGCGCAGGAGGGCCGCGCAGGCCCCTGCGCAGGCGTTGG
GCGGGACTGCTTCCAGGTGTCATAGCGGAAGAACTTGCCCACGGGGTATCT
GGGGAAGTTGTCCTGAGAGGGGAAGGGCCCGTCAGGGGGGGGCCTGGCCC
CCCAGCCCCTGTCCCAGAACAACAACCTTTGCGGGGTCCTCCTGCCTGCC
Contig 50 (179 bp)
ATCTTCATATTCATGCAGAAGACACTCTCCTGCCTTTCTATCTTGGGGAA
AAGGACGATGTCACTTATGCAATAAAGCCCACTTGCTGGCCGGGGCTTGA
CATTATTCCTTCCTGTCTGGCTCTGCACCGTATTGAAACTGAGTTAATGG
GCAAATTTGATGAAGGTAAACTGCCCACC
Contig 51 (500 bp)
CTCGGGGCTGCTTCCAGGGGGCCTTGGGGAGCCATAGAATGCTATGGAGCA
AGAGAGTGCTATGGTCAGACGACTTTGGGGGAAGGTCTGGGAGAAGAGGG
GTGACTGCCCACTGTGATAAAGAGTGGGCGCTTCCTTGAGATAACACGGT
GGGCAGCCGAGGTGGACCTGTGCAGGTGGAGAAGGCCTCCTGCCGCGGCC
AGTACGTGGCTCTGGGCTGCCGGACACGAGAAAGCCCACCTCCACGGCTG
CCTCCAGGCGGCCCTTCCTCTCTTCACACCGCCGGGCCATGCCCAGGTGC
AGGTGCCATCAGAGGGTGCTCAAGAGAAGCTCTGGGCTGGGGTTGTCCCA
GGTCCCGGAAGCCCCGTGTCCCAGGGGCCCACCTGAGGAAGCGTGGGCGCA
CAGAGACTGTCCCTCGGTGCTCAGAGAGGGTCCCGTCCCCACGGCAACGA
CGCCCAAGGCGGAGGTGGTCAGAGGTCTTGGGAGGGAGGATGGCCGCGCA
Contig 52 (900 bp)
TGTGTTGCACCTGTTGCTGCCTGTCGACTCTAGAGGATCAATACTCCTTA
CATAATTAAGGAGAACAAAATGGAACTTAAAAAATTGATGGGACATATTT
CTATTATCCCCGATTACAGACAAGCCTGGAAAATGGAACATAAGTTATCG
GATATTCTACTGTTGACTATTTCTGCCGTTATTTCTGGTGCAGAAGGCTG
GGAAGATATAGAGGATTTTGGGGAAACACATCCCGATTTTTTTGAAGCAAT
ATGGTGATTTTGAAAATGGTATTCCTGTTCACGACACCATTGCCAGAGTT
GTATCCTGTATCAGTCCTGCAAAATTTCACGAGTGCTTTATTAACTGGAT
GCGTGACTGCCATTCTTCAGATGATAAAGACGTCATTGCAATTGATGGAA
AAACGCTCCCGGCATTCTTATGATAAGAGTCGCCGCAGGGGAGCCATTCAT
GTCATTAGTGCGTTCTCAACAATGCACAGTCTGGTCATCGGACAGATCAA
GACGGATGAGAAATCTAATGAGATTACAGCTATCCCAGAACTTCTTAACA
TGCTGGATATTAAAGGAAAAATCATCACAACTGATGCGATGGCTTGCCAG
AAAGATATTGCAGAGAAGATACAAAAACAGGGAGGTGATTATTTATTCGC
TGTAAAAGGAAACCAGGGGCGGCTAAATAAAGCCTTTGAGGAAAAAATTTC
CGCTGAAAGAATTAAATAATCCAGCGCATGACAGTTACGCAATGAGTGAA
AAGAGTCACGGCAGAGAAGAAATCCGTCTTCATATTGTTTGCGATGTCCC
TGATGAACTTATTGATTTCACGTTTGAATAGAAAGGGCTGAAGAAATTAT
GCGTGGCAGTCTCCTTTCGGTCCATAATAGCAGAACAAAAGAAAGAGCTC
Contig 53 (450 bp)
CCAGCCACCAGCTGGACCCTCCCGGAGAGGGGCTGCCTCCTCTTTCCCGC
CCAGACGCCCCCCAGCAATCTGTGGCCAAGAGGGAGTGATACCGAAGATG
GCCACATGGGGGCGCCAGCCCACAGGGAACCCCAGGAAGGCGCTGGACCG
TCAGGAGTCAGGGCTGCTGTGCACCCATGTGGCCTGGGGACTTTCCACAG
CCTGGTGGAGATGGCCGGGCACACCGCTGCCTCGGGGGAACGTGCACACG
```

FIGURE 6, CONTD.

```
GGTGGTACATGTGGCCGGAGCCCAGGGCACAGGGTGAGGGGAGAAGGGAG
CATGCGGGTGCAGACTCGGAGCCCGCGCGTGAGGTGCTGGGTCCTCAGGA
CACGCTCTGGGAGTGGAGGACCCCCATCCACGCCCTCACCCAGTGTGTGC
CCGCCTGCTCCCCCGGAAACCCTCACAGACACGAGGGCACACCCAGCCCC
Contig 54 (1133 bp)
ATGGCGCTCATTAGAATTCGACCTCGGTACCTTGGGATCTTTTGACCCCT
ACCTCACGCCATCTACAACATTTACCTCCGAATGAATGAGAGACACCAAA
AGCAAATTCATAGAAGAGAAAAAAAGGTAACCTGGACTTTAAAAATGTAA
ACTTCTGCTCTTTAAAAGGCAGTGCTAATGAAGTTCAAATACAAACCACA
GACCATAAGAAAATACTTGCAAATCTTGTTCTGACAAAGACTAGTGTTCA
GAACATACGACGATCAGGGAGAGGAAAACCAGCAATCCTATAAAACTGGA
CAAAGAATTGGGGGGAAAAAAAACCCACTTGGCCAAGAAGTTGGTAAATA
AGGCCATGAAAACATGCTCAACATCATGAGTCATTAGAAAAATGCAAATT
AAAATTATAATGAGATACTACTACACAGCTATTTGAATGGATAAAAAATG
TTTTAAAAACTGATTATACCCAGGTTTGGCAAGAACATGAGAAACGAGAT
TTTCACACACGATTGGTGGAAAACAGAAATGGTCCACCCACTTTGGAAA
AGAGCTGGGCACTTCCCTCAAAAGTTAAACATACATCCAGGACCTCACAC
AGGCTTTCCACCACAGGTGTTTATTCCAGAGACATGAAAGCGCTCATCCA
CACAAAGACTCGTAAATGAAGGTTTATAGCACCGTTTGTGGCCCGAACTG
AGAAAACCCAAATGACCTTTAACCAGAGAATATCTAAACAAAATATCCAT
TCACATTAATCACCCATAAGAAGGAACGGGCTATGGGGACGGGAACCGTA
TTGAAGAGGGTCAAAATACATACGCAGCATCAAAGAAGCCTGCCCAAAGG
ACACACACTGCAGGGTTCCATGGACTGAAACTCGAGAAGGTGAAAACTCG
CCAGCAGTGACAGAGAGCAGGTCCGAGATCAACCTGATGTGGAGGAAAGT
GAACCCTCGTGCGTTGTTGGCAGGACTATAAACTGGAGCAGCCCCTACGG
ACAACAGTAGCCCGGGCTCCTCTCCTCCATCTCCCTGGGGAGCCTGAGCC
TTGAGACGCTGGGGCAAGTGCACGGCATGCTGCCTCACGTGGGGCCCCGG
TGAAAACACCTGGCAGCTGGGGAAAGAATCGTA
Contig 55 (735 bp)
TACTGCCTGTCTCTATGGACTTGACTCCTCTCGGGACTTCATGCGAGCGA
TCTTACAGAATTTGTCCTTTTGCATCTGGCTTGTTTCACTGAGCATCGTG
TCCCCAAGGTCCATCCATGTTGCAGCCTGTGTCAGGATTTCCTTCCTTTT
CAAGGCTGAATAGTACTCCACTCTGCGGATGGACCACGTTTTGATTATCC
ATACTAGTAAATCCATACTAATAACTTGTTCACTGAAGCCCACAGCTTAT
GCTACCTTCCGTGGGCTCCTCCCTGCCCTGTCTCTACGCCTTCTGCTATA
GCCCCATCCCCTCTCATCCAGGCCACGCCTCCTGTCCCCTGGACACTGTC
CCAGAAGCCAACTGCCCTCTGACTGCTGCTCTCGCCTGACGGAGGACAAG
GCAGGCTCAGGGGTCCACGGGCTGGGGCCCCAGGGCTCCCCATGGCTGGT
GCCCCTTCCTGATTCCAGAAGTACAGTGGCAGCACCAGCTTTCCAGCTGC
CCCACCTTCTGTCCGCAGGCTGCTCGGGTGGGGGCAGGTGGGCAGTGATG
TCACCTGCTGTAACCACCCTACCGTCGCTCATCCCTGTCCAGGAGGTCAC
GGTGACCTTGGCAAACATTCTGAACAACACACACCTCCCTCTGCTTAGAG
GCCGGGGGGCCTCCCCGGGTGACTGGGGGCACAGGCTGACCCCAGCCTGTC
TCTCTTCTCTGAAGGACATGATAAGTACTGCAACA

Contig 56 (500 bp)
AGGAAGAACAGGAAACAACGGGGTTGAGGAGAAGAAACGGGTGTCTGGCA
GGGGCACGTGCCAACGGTCCACCGGGTGCTGCCGCGCTGCGGCCTGGCGC
CAGAGGGGGCAGCTCCGCCCCTCGGGCCGCGCCCTGCCGCTTGTGCTGGC
TCGCGGCTGGGCTCTGCTTGGCTGGGTTACAGCTGGGTGCAGCCGCAGGC
TGTGGTGGGTGCCGCCGGGTCAGCCAGCCCGGCCCCACCCGGCCCGTCTC
GCCGGCCTGGCCCGGGCAGCCCTCCTGCAGTCGAGGAGTCGCCCTGACGG
GCTGATTGGTCCACAGCCTCAGATGCAAACCAGCCCCACGTGCCTGGAGC
CAGCCAGCCCGGGACACCCTGGTGGAGGCAGGAAGGCAGCAGCCTGGAGA
GCCGCGCCGGATGATGCTGCGGGGGAAACCGGGCTCCCGCCGGGGGCGCCC
TGGCTCTGGCCAGGCTTGCCTTGAATGCTGACGTGAGCGGTGGCCCTATA
Contig 57 (500 bp)
TGGCGTTGCAGTGGCTCTGGCGGAGGCCGGCGGCTACAGCTCCGATTGGA
CCCCTAGGCTGGGAACCTCCATAAGCTGTGGGTGCAGCCCTAAAAAGCAA
AAAACCCCAACATATATATATATATATATATATAATTATGGTAAAATACA
CATAAAATAGAATTTACCTTCTTAATAATTTTCAGTGCACAATTCAGTGG
CACTAAGCACATTCATGCGGCCGTGTCACCTGCTCCAGAACTTTCCATCT
ACCCAAACGGACTCTCCGCCCCATGGAACACGCCCCCTGCCCCTCCCCCG
GCCCTGCCCCGCCAGCTCCTCCCTGTGTCTGTGGATCCGGCTCCTCCAGG
```

FIGURE 6, CONTD.

```
GACCCCGTGCGTGGGCTCACAGAGTGTGTGTCCCTCTGTGACCGATCGTC
GTGTCCCCGAGGCCCGTTCTGTGGCAGCTGCGTTATGACCGACTACCTTC
GAATGCTCAGTGACTGCCGTGCATTGGACACGCAGTCCGCTACCCTTTTC
Contig 58 (550 bp)
TGCTTTCTGTGCCCCCCTCCAGCTTGGGACCCCAGCAGGGCAAGGGGTGT
ATAGGGCTTAAGGAGGCAGGGGCGTCTCCTCCCGCTGGCTGCCCAGAGC
ACCCCCAGCCCCGCCTGCCCCTCGTCCATCTCCAGCCTGTCCTTTCCTGT
GCCCTCCCTGTCCCGGGCGGGCCGCACACTGGCTTCCACCTCCCCACCCA
ACTGGCGGCCCGGTCCTTCCTGCTGAGGCACCCCGAGGTCCCCGCTGCTG
GGGACCAGCTGGCAGGTGGGTCCCACTGCTTTCTCAGCGTGGGCTTTGGA
GGGGGGATCTGCACATACCATCCCTTCAGGCCCCGTGGGGAGCCTGGGGA
CCATCCGGGACCCCTGTGGGCAGGCCCAGAGGACTGCCAGGAAGAGACCC
AGGGGACCAGGCAGCTCCCAGGCCTCTCAGCTTCAGGCCAGGGGAGCCCA
CCCCCAGGTGGCAGGTGAAGCCAGGCCCCCAACCCACAAAACTGCCCGCA
GGGAAGTAGGAGCGGACAGGAGGAGGGGAGGCCAGGCCCGGGCCGCCCTTG
Contig 59 (800 bp)
TGAGGAGCGCAGGCCCAGGCCTGAGTGTGCCCAGCTTACACCCCTGGCAG
CTTCGTCCCTCCTGGCCCTAACCCCCATCCTACCCCAGCAGCAGGGGCTC
CCCCGGTGGGGCCTGCTGAGCGTCTGACTGGGGTTTGGAGTCAGGTCTGC
TCCAGGCTCAGCCCCCATCCCCAAGGGTGCCCTGCAGCACTGCTGCCCAC
CCCCTAGCGCCCCAGACCTTCGCCCCTCCAGCCTGGATGTACCCACGGA
CCCTGAAAAGTGGGGCTGAGCAGGTGCCCTGGCTGGAGTCCCCCTGACTT
GGGGCTGGCCAGGCTGCCCTGGAGGGGCTGTGGGGGCACAGCCTGCCCCA
GGGGCCCGCTGGGCACTGGCTCTGGAGCTCACGACAGGCAGGCCCTCTCT
TCCTGGCGGGGCCACACCCTGCCCTGGGGTTTGGGGCCAACGCGGGCACG
CCCCATGTCAGGCGGGGGCGAACCAGGTAATTACAGCCTGGCAGCCCGCT
CCCCAGACCCCCAGCCCCGGAGGGCCCCCACCCAGGCTGTGCCACCAAGA
CCTGGCATCCAGGCCCCAAAGCAGGTCAAGGGCAGCTGCTACAGATTCTT
TTAAGTTGAGACAGAATCGACACATGACAAGTTCCTGGTTTTAGGTACTT
CGCTGCCGGGGCCGCCAGTCAGTTTAGTGACCCAGCACACCCCACACAGG
TACAATTGCTCTTCTCAAAAGAGGCCCCTGAGAGAGCCGCCTGTCTTGGCT
CAGGGGTAATGAGCCCAATGGGTATCCATGAGGTTGCGGGTTCCATCCCC
GGCCTCGCCGCGCGTTGGTTA
Contig 60 (500 bp)
GGCTCAGCAAGCGCAGGGGCAGCGTGTGGGGCGACGGGAACCATGGGGGT
CTGTCTTCCCGCCTCTCCTCAAGCCCACCGCCCTGCTGCCCACCTCCGAC
TCTGCAGCCAGCATGCCGGCTAGAGCCCCTGTGCACCCAGCTGGTGGCCT
CTGGCTAAGGGCAGTGCTGGCTGTGGACGCGTGTCCCCTCCCCAGCAGCC
CAAGGGTCCCATCTGCCAGGCTGGTGGCTGAGGTCTGCCCTGTGTGGTCC
TTGCAAAAACCCCGCCCTCTCCTGCCCCTTGAGGCGTGAGGGAGACGCGG
GCTGGGCGGATGCCCTCGGGCACAGCCGCCCGCGGTGGCGCCCTGTCGAG
GAGGGGGCTCCGACGTGCCCTGACGGCCCTGGCCGGGCGGAGAGGGTGAG
GCCACCTCCTGGCCACGTCCACCCAGCTGCCACGCCGCCTAGCCAGTGGC
CCGGGGGCCAAGTCAGCAGAGCCCAGCCTTCCGACAAGCAGAGGCTGTAGGC
Contig 61 (700 bp)
GATGAGGAAGCCGCTGCTCGTGCTGCTCGTCTTCTTGGCCTTGGCCTCGT
GCTGCTATGCTGCTTACCGCCCCAGTGAGACTCTGTGCGGCGGGGAGCTG
GTGGACACCCTCCAGTTTGTCTGCGGGGACCGCGGCTTCTACTTCAGTAA
GTAGCTCAGCGGGGCACGGGGGCGGGGCGGACACAGCAGGTGCTCCATCG
GTGCTGCCCCGGTACCTGTGCGGGTCCTTCGGGATGGATGGTGTGGGGGA
CGGGGGGCGGGGGGCGGCCAAGGGAGGACCTCTCCTCCGAGGGTCTGAGA
CTTCAGACCGGGGGCGCCCTGGCCGTGCGCATTGATTGGCACCTGCCATG
TGCCTGGCTGGGGCTCACACCCCCTGACGTTCCTGCAGCGTGACTCGAAA
CGGGAAACCGAAGGGACGGGTGGCACGGGGTGGGGAGGCAGACCGTGAGT
GGCAGGCGTGCGAGGGGTTCTTTCGGGCGGGGTGGCCCAGGCAGGCCCCA
CAGGATGACAGCCTGTCCCCTCCTGCTCCTCCTTGACCTGCCCACAGCCA
GGGCTGCAGGCACTGACATTCACCCATGGTATTGTGGTGCCTTGACGTCT
TGGCAGTGGGCATTGGGTTCATGGACTGTTTGGATTGAAAAGTGGGAATA
AGATGGGGTTTGAAAAACCCAATTAAGAAATAAAAGGGCGCCCTGTGGGC
Contig 62 (300 bp)
TTTGAAAAATTTTGAGTCAGTGCAGAATTCGCATCTATTCCGCATTCAGG
CTCTCCTGTTCTCACCTTGCCTTAGTGCGGATCTTCTATAACCACCACAG
TGACGTTTTCAAGGTACTTTATTGAATAATAAGAAAAAAGTGCACACAAT
CATGTAGTTAACTTTCTGTGCTCTTTGCCAGTTTGAAGGGACCCTCTTTT
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
TTTCCTTTTTAGGGCTTCGCCGACGGAAGTTCCCGGGCTAGGGGTTGAGT
CAGAGCTGCAGCTGCTGGCCTACAGCACAGCTCTTGGCGGCGATGGATCC
Contig 63 (450 bp)
TCCTGGGCCACAGGCTGCAGCAGCTCACCTGGGGGCTGGGGTCTCGCTCT
GCGGATGGACCCATGAAGGCCGGAGCCAGGTGGGGGCCGAGACGGCAGGG
CAAAGGGTCTGCACACACAGCGTCCCCCCGACCCGGCTTCTCTGGGTTCT
TGGGGGGTTGGCGAGGCTTCTCTCAGTCTGGGTTTCCTGGGGAACTTTCA
AGAACTGGGAAGTCTTCCAGAAAGTTGGGGTGAGGGGAGGTACCCCCAAA
GTGCTGCTCCTGTCCCCATCCCCCACCCCGCTGTCCATCGGCGAGACCCC
GGACCGCCGTCTCCCTGCCGAGGTGTGGGGTCCCCCCCTCTGCCGGCCAG
GCTGGGCAGGGGTGAGCGCCCCCTGCTCTGCACTCGGGACTCAGCCTGGC
GAAGGCGGGCCCCAGGAGGTCCTGGCCTGGACGGCAGTGACCTTCCACCG
Contig 64 (500 bp)
TGTGCATCCAACCCCAGTGGCCACGGGGGGTGACCCTCGGCCGGTCAGCC
GCCCGCGTCTCCCACGGAACCGGGCCTTGGCCTGAGGCAGAAGGACCCAG
GACTCCATCCCTGCCCCGGACTCTGCCGGAGGGTGCGGTCTGCACAGAGA
CCCTGTGGGGGTGAGGCCGGTCGGGGCTGGGGTTGAGATGGGATGGTCAG
GGCGGCCCCCGCGGGCCTGCAGGAGGCTGGGTGAAGGAGGGGGCCCAGCT
CAGACGCCCCCAAACCTAGCTTGGGAGAGCTGCAGCCCCGCCCCGTCAAT
CGCGACAGCCTGCCCACAGAAGGCATTCAAATGAGAGACAAATATTTGGG
CTTGAAGACTATACCCAGCCACGTCTCTTTGGGAGCCCAAGCTGCTCCCA
GGCCCTCATTTGGGTATTAATTGGTTTTCGTTTAGAGATTTGCATGCTTA
TCAATGGCCACTGGGCGGCTGGGCCTGGATGCGGTCCCAGGCTTTGTATG
Contig 65 (661 bp)
TCCCACGACCTGCCCCTCCAGGGCCACATCTGGCGACACCGTCGGCAAGAG
TTCGACCGGCCTGGTGTGGCCACAGCCTCAGGCCTTGTCTGGCCGCCCAG
GCCGGCTCCAGGCTCCAAGGAGCTCCTGCCTGCCCTCCGGAACCCCAGCA
CCCCGGGCCCGCTTCCCCACCAGACCTGTTTTTCCAGGTCAAGGTCACAG
CTAATTTGGGCTTAAACTGGACAAGGAGGCCTTATCTGGAGCAGGCTCCC
GGCCCTTTGGCCTCTGCCCTGGTGGGGAGGCCTTCCCAGAGGCTGTGTGT
TGGCGCTGACCGTGCAGCCCTGAGCTTGAACCCGGATAAGGAGGGACCCC
ACCTGGGCTGGAGCCAGAGAGCCCTCGTTCCCCAGCTCCGCAGGGTTCTC
ACAGTCCCGCCCCTGCCCTGGGGACCCTGGACCTCCCCAGCAGGTGAAAG
GTCCAGATGCCCTCTGACTAGAGGCTCCTCCGCTGTCAGACATGCTCCCT
TCCCGCACCGAGGACGAGACCTCAGCAGCCCTGCGTGGCCTGGGGTGCGG
ACCCCAAGGCGTCTCTGAGTGTGTTCTAATGGGGAGCCGTGGGGCCTCAA
CAGTGGGGGTGGCACTTGGAGGGGGAGCCTCCCCACAGCTGCCCCAAGATG
GGCCCTGGACT

Contig 66 (500 bp)
TTTGTTGGATGAATGAAATCATGAGAAAGTGATTGGACCGCCCCGTTCCT
CCAGCTGCTTGCCAGCTGCTTTGTAAAGATGACCTCTCACCTTCTCAGAG
GCCTGGCCGGCCCGAGGTGGCAGTCAGCTGAGATGCCATGCTTGTTTGGC
ACGTGGGAGGCCCCTGTCCACGGCGTGGGTGCCTCTTGTGTCTAATCAGG
GTCAGGGGGAGCAGCAGGTGCAGGGCACATGTGGGGCCGGGGCCGATGTC
TGGGGAGGGCGGGAGGAGGGGGTGTGCGGAGGCCGTTGTGGGGGTGCAGG
GGACAGACCCCAGCGAGACCCTCCCTGGCCAGGCACCAGGACAGGTGATG
GGGCGCCGCCTCCGGGGCGTGTGACAGAAGCCTCTCAGAGGAGGCCCTCC
CACGGTCTCTGGACCATCAAGGGACCGGGGGCGCTGGGCCTGGGGGTCAC
ACCCAGCTGGCCGGCCAGCCCGGGTGGGGTCGGAGGCCCGGGCAGTTCAC
Contig 67 (550 bp)
GGGCAGGAGGGGCCCGGGGCTGGTGCGGAGGGTGGAGGTGGTGCAGGAGG
GTGTGAGGCAGGGCTCACTGAGCGTGCGCGGCTGGCTGTGCCCTAGAGTG
GTTAGCACGTGCCCCCACCCTCCAGTGTCGCTCTGTTCACCTGTGCCTGG
CTCACAGGTGTGGAAACTGAGACTCGGGTGTTGCATGAGCTTCCAGGATG
AGAATCAGCAGGCTTCCCAGGCAGGGCTGTGTCCGGGGCTCTGGGCTCTT
ACCAAGGAGGGGACACCCAGGGACAGCCCTGCTTGGGGGTGTCGGGCTGG
CCAGGCTGGGTGGTCCTTCCTGTGGCTGGCAGCCCTTGGCAGTCACCCCC
TTACCCTCAACTGCCCCTCAGCTGAGACACGACCTCCCTGCAGAGCCCTG
TCCACCCAGACACTCACTCGCCTCCTCCAGGAAGCCTTCCAGGGCTGCCT
CGCCCTGGTCTCAGCAGGAGACAGAGAGAGAGGGTGGGCCCAGGAGCAGA
GGCAGGCAGCCAGAGGGGAAGCCCAGGGGCCCTCACTCACCCCTGGGGCC
Contig 68 (500 bp)
TTTGCATTCAGCTCGTACCCGGGATCCTTCCCGGGGGGCTCTGGGGGTGGG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
GGAATGGGGGTCAGAGGCAGCTGTCATCTGCCTGTCCTACCTGCTCTCAC
AGGCTGGCCCTGGAGCCCTGGCCTCCTCCTAGGGGCACATCAGGTTTTGG
GGGAGGCCCAGCCCACCGTCCCACCTCCAAGACCACAGCTGGGAGCCTGC
CCCCCAAGCCTAGACCTAGTGGGGCTCCTGCCAGCCAGGCCCCCCACCTTC
ATGCTGCCACCCACCAAGGTGGGACAGTGCAGCCAGGACATCCAGCTTCT
GGAGCTGCCCGAGGCTCAGCACAGGCTGGTACCCTAGGGAGCAGGTCACC
CAGGGCCGCCTGGCGAGGCCTGCGGGGACGGGGGGTAGGGTGGGCAGCAA
AAGAACCTCTGAGCTGGGCCGGGCGGGGTCGGTGAGGGCCCGGGGCCGCG
GGCTGTGTGCGTGGCCCCTGAGCCCGTGCAGACGCAGACCCTGGGTGGGT
Contig 69 (550 bp)
TGTGCTGCTGTGGCTGTGGTGTAGGCCGCCAGCTGCAGCTCTGATTCGGA
CTCCTAGCCTGCGAACCTCCATATGCTGCTCTAAAAAGACAAACATAAAA
TAAAATGGGTGCGCTGTTAATTTGAACACTCTGCCTCCTCCAGAGACGAG
GCCGAAACAGGCCTCTCTGAAGGTCCCACCTGGCAGGGAGGAGGAGGCCA
GCCCCGTGGGGGGCAGAGAGAAGCCCGATGTCCCCAGACACACACGCACA
GGGACCGTGGCCCCGGCTGCCAGCCCCGCGGGGGGAGGGCAAGGCCAGAG
ACTCCCAGCAGCCCACAGGACCTTGGTGGCCACAGGACACAAACACAGGT
GACGGTGGGTGAGGCCTGGCCTTTCCCCCCCTGGGCACGAGCACAGGACA
CACAAGAGCCCCAGCGTGCTGACCGCCACGCCAAGGAGCCTGGATGAAGC
TGGACACCGAGAGTCCACACTGTGTGATTAGGCTGACGTGAAGTTTAAGA
ACAAGCGGGTGGCTCAGCGCTTGAAGGCCAGAACAAGGCCGGCAGGGCAG
Contig 70 (1300 bp)
ATGTCAGGATAGTAACCTGGGGTGCTGCAGTGACAATGCCAGATCCTTAA
CCACTGTGCCACAAGGGAACTCCTTGACCTAGAATCCTATACCCACTGCA
AATATATTTCAAAAAAGGTAAAGTCCTGAGCAGAAAACCAAAAATGGGAT
AATTCATTTCTGGAAGACCTTCCTTGTTAAAGGAAGTTTTTTGGACGTGA
TGAAGGTAGAAACTCGGAGGCACACAAAGAAAGAAAGAAAGAAAGAGCAC
TGGAAACGGAGCAAATAAAGGTAAAAATAAAGTTCATCTCTTTCTCATTT
TTTAATTGCTCCAAAAGATAGCTGACCTCTAAAGTAAAAAAATAGTGGAAA
TGTAGCATATGTCTCTAGCGTAATTTAAAGTATAACTTATAGCAATGATA
GCCCAAATAAAGGAGGAATTGAGAATATACAGTTGCTGTGTGTTCCCATTGT
GGCTCAGCAGTAATGAACCTGGCTAATATCCATGAGGATGCAGGTTCAAT
CCCTGGCCTCACTCAGTGGGTTAAAGGATCCAGGGTTGCAGTGAGATGTG
ACGTATGTCACAGACGTGGCTCGGATCTGGCATTTCTGTGACTGTGGCTG
TGGTGTAGGCCAGCATCTGCACCTCCGATTTGACCCCTAGCCTGGGAACC
ACCATATGCTGCTGGTGTGGCCCTAACAGACACAAAATAAAATAAAAATA
AAAGAGAGAGAGAATATACCATTGTAAATTTCCTCACATGACACAAAGAG
CAATGTGATATTATTTGGTATATGGTGATTGATTCAAGATGTATATCATA
ATATTGATTCAAGATGTATATATTCCTTTTCTAAAAAAGAGATTTATACA
ATAAGGCAAGAGTGAAAATAAAGTGGAATGCTAAAGAATAGTTAATCCAA
AAGAAGGCAGAAAATGGGGAAAAGACATATAACAGATGGAACAAATAAAA
AAGAGCTAATGAGATTGTAAAATTTAATCCAAACATACAGATAATCCCAT.
TAAATTTAAACACTCTCAACACATTGATTAAAAGAAATTGTCAAATTGAA
TAAACAAAGCAAGACCCAACTAGATGCAGACTATGAAAAACCCACTTCAT
ATAAAGACATGGGTAGGTTTAGAGCAGAATGATGGGGAAACCATGTCACG
CAAACATTTGTCAAAATAAAGCTGGTGTGGCTGTATTCATCTCAGACACA
GCAGACTTCAGAACAAGAAACACTCAAAGGATGAAAGAGATACTGCATA
ATGATAAAGGGATCAATTTTCCAAGTGCAGGCTCCAAACAACAGAGGTTT
Contig 71 (500 bp)
ATGACCTCATACTGAATCGAGCTCGGTATCAGGGGATCTCTCAGCTGGGG
GGGAGGGCAATGGGGCATTTGTCTGAGGATGCCCCAGGGCAGGCCCATTG
GCTGGTTTGGTGCCCATGCCCCCCCCACACCCCGGCAGTGCCCCCTGCTG
AGCCTGGGACCCCCTCTGGGAGTTAGGGATTGGGGGTGGGAACCAGGCTT
TGCAGTAATTCCAGCCCCCAGGGCCCTTCCCTCCCCGCCCTCAGGACCCC
CAGCCCCGCCCCACACAGTCTCCACTGTGACAGCCTCACCCCTTGGGTCA
AGTCCTGTCCTCTCCGGCCCCCGCTGGGCAGTGGAGCCAGCTAGGTGAGA
GGCACAGGCCACTAGGGCGGTGGGCACTGCTGAGGACAGAGGGGCCTGGG
TGGCCTTGGACGAGGCCCAGCGACGCTGAGACAGTGAGCCAGGCTCCAGG
CTTTCCCAGGGAGGGTCCCTGAATGTCCACTTCTTGTGACATCGGGTGAC
Contig 72 (550 bp)
AAGTCCATTAGGGAAGGGATTTGTGCAAACACAGAGACAGGTGCAGGGCT
GGGCCAGCTGCTGGGCTGGGGGCTCCTCAAGGCGCCCGTAAACCCCTCCC
TGCCAGCCGCCTGCCGCCAAGGTCTGCTGTCCACCCCGGCCGGGCTGCTG
TGTTCCCGGCGTGTGTCCTGCGAACCCGACTCCCGTTCACCCCTGAGCAC
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
TGCCTGGAGGCCGGCTGCCCAGGCGGGACGGGCCCTCAGGGCTGGGCTGG
CTCTTGGCCTGTGTTTCATTTCTGAGCAGGTCCTTCTCAGTGGGGGGGGC
CTTGGGTGAAGCAGGCATGTGCACCACTGGGGCCCTGTCCCCAGTGGGCA
TCCTGGGCGCTTGTCTGGCCCCCAAACCCCCAGGCCGTGTGCATCATACC
TTCACCCTGAGCCCCAGCCGAACCCCGGACATGTGCTGGGGGACCCTGGG
CACAGGGGTGAGGGAGCAGTGGCCTTGGTGGAAGCCCAGCCTTGGCACCT
GGGGAGGGGGTGCATCTGGCATGCTCTGCTGTAACCAAGCCCAGGGCAGG
Contig 73 (950 bp)
GACGTGCAGTAGCCATGACCTCTACGGCCCCCACTGACCAGCCCGTGTCC
TTGTCCCGAGACCGACCCCTAAGCAATAGGATGCAGCAGAAGTGACAGAA
CGGCCTCCGCGATGAGGTCGCAGAGGGCTCTGGCTCTGACTCAGGCCCCT
CATCCCTCGCTCTCCTGGAGCAGGGCCAGGTAGGGGCCCCCCAGAGACGC
CCTAGAGGAGGTGACGGGCAGCCAGCCCGCCCCAGGGAAGGCCTGGGGAC
ACCAGGGAACAGAACGGCACAGGCTCCTGGCACAGTCTCCCAGGAGCCCC
CTGGTGGCACAGAAATCCTGACCGGCCCAGTGGAGGGGGCTGGGGCGGGG
CTCGGGGAGGAGGGACTGGGTGAGGCCGTCTGACTCCTGGCTGAGCGCCG
CATACTTGCTGCCTGCCCACGATGCCGGGCCAGGCCTTCCGCACGGACCC
AGGCTCACATTCGCCCTACATGCCACTGTGTGGGAGTTTGGGATGGTGTG
CCCGCTGGGCCCGGGGGTCAGGGCACGCTTCCCAGAGGAGCGGGTTCCAG
AAGGCCCAGGTGGACAGGCGATAGGAGGGCTCCAGGGGGCTTCCCAGGCC
ACCTGCGAGGACCCTCCTGGGGGGAAGGGAGCGGAGGCAGACAGCCGGGT
CCCTTAGGCCAAGGCTGAGTTGTGACCGCAGGGAGAGGAGAGAAGGAGCA
CCCACAGCAGGGCAGGGGCTGCGGGAGGCTGTGCTGGGTGGCCGGGTGGT
GGGTCTGGGGGCCAGGACCGTGGGAGGCCTCGAGGGGGGAGCAGGCACGG
GAGGGGCCCCTGGACGGCAGAGTCCCTGCTCCAGCTGCCGCCCCGACCCC
AGGTCCACCTTCATTTCACAGCCTGGCCCCCGGCCGCTCTGACCGGCCCT
GCCCATGCAGGTGTAGCGGGGCAGTGAGGGCCAGGCTCCGGCCGTCCCAA
Contig 74 (450 bp)
GCAGGCCTGGCAGCAGGGAAATGATCCAGAAAGTGCCACCTCAGCCCCCA
GCCATCTGCCACCCACCTGGAGGCCCTCAGGGGCCGGGCGCCGGGGGGCA
GGCGCTATAAAGCCGGCCGGGCCCAGCCGCCCCCAGCCCTCTGGGACCAG
CTGCGTTCCCAGGCCGCCGGCAAGCAGGTCTGTCCCCCTGGGCTCCCGTC
AGCTGGGTCTGGGCTGTCCTGCTGGGGCCAGGGCATCTCGGCAGGAGGAC
GTGGGCTCCTCTCTCGGAGCCCTTGGGGGGTGAGGCTGGTGGGGGGCTGCA
GGTGCCCCTGGGCTGGCCTCAACGCCGCCCGGTCCCGCAGGTCCTCACCC
CCCGCCATGGGCCCTGTGGACGCGCCTCCTGCCCCAGGCTGGGCCCTTGC
TGGCCCCTCTGGAGCACCCCGCCCCCCCGGGCCCAAAGCCTTTCATGAACA
Contig 75 (1363 bp)
CCTCCAGCTGGGCCCGGCAGGGCACCGTGCCCCTCAGGGGACACCACGGG
GGGCCACAGTGGCCTCTCCTGCTCCAGGCTCTGCTCCCGCCTGGGGCCCC
CTGGGCCGCCCGCCCATGGCCAGGGCAAACTCCCAGTGCGGCTGCCCGTC
TGGGCAAAGAGGCCGCCAGGCCCCGCGTGGTCTTAGCAGGCACTGGCGGA
TGCCGNTAACTAACCATTTCTTCCGCAGGAGTCCGAATCTGCTCTGACCA
CGGGCCCTAAAAATCGCTCCTGGCCCCGCAGAGGATCCCCGAACAGCGGGC
CTGCCTCCTGCTCCTCCTGCCGGGCCGGCACTCGGCAGGCACGTGCCCTC
GTCGTCCCCAGTCTGTCAACCGTCCCGTCGTTACGATCCCCAGAGTCCCA
CGCGCGGGCAGCTCTTTCCACACCCCGCACGGCCCCGGAGCTGCCTGGGC
ACCCAGATCGCCCCTGACGCCTTTGCTCCTAATTCTGCTGAAATACACAT
AACGTCTCCTTGAACGTTTGTCCATTTTCACGGGGACAATTCTGTGGCCG
TAGGTACACTCCCCTTGGGGCGCAGCCATCGCACCATCCGCTTCCAGGAG
GTCCCGTCGTCCCAGATGGACACTGTCCCCACTGATCCCTAATTCCCTGT
CCCCCCCAGCCCTGCCCTTCCTGTCTCTGTGGCCCTGGCGCCTCCAGGGA
GCCCCTGTGCGTGGGATCACAAAACGTGTGTCCCTTTGCGTCCGGTGTGT
GTCTCTGAGCATCCGGAGCTTGGGGTGCTTCCACGCTGCGCCTGTGTCAG
GACGTCCTTCCCTTTTGCGGCTGCGCGATGCTCCCCGTGGGGCTGCCCCA
CACTGCGCGTGTTCGCTCATCCATCCACTAAGGCTGAGTTACTTTTGGCG
GTTGTGAATACTGCTGTGTGAACACGGGCGTGCAAATACCTGCTGGAGGC
CATGCTCTTAGGCCTCTCGGGGGGCACACCCAGAGCGGATATGCTCAATA
AGGTAATTCTGTGTTTAGCTTTTTGGGGAACCATCAGGCTGGTCTCCAGA
GTGACGGAGCATGCGTCGCATTCACAGGAATGGTGCTCGAGGCTTTGAGG
TCTCCACCACTCGCTTCCTATTTTCTGTGCGTCACAGCCGTCGGAACGGC
TGGGTGGTGCCTCTGTGTGGCTTCAATGTGCTTTTTCTTTTCCTGGCTAT
GAGGTTGAGCGTTTTTTATGTACTTGCTGGCCATTCGCAGGGTTTTTGGG
GTTTCTTTTCTTTTTTGCCTTTGGGGACGGCGCCCAGAGCGTATAGAAGT
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCCCTGGCTGGGGACTGAATCAGAGCTGCAGCTGCCAGCCTAGCCCACAG
CCGCAGCAACGCA
Contig 76 (500 bp)
TCATGCCATCGCCACCGCCCCCCACCCCGACGTTTCAAACACCAGAACCA
CCCCTCGGGCGGCAGAGAGAGGACCGGAAGGAGAGACAGCCTGGTCCCAA
GGCCTCGCCCGGTCCTGTGTCTCCGAGCGACATTTCTTTCTGTTTCCCTC
CTCCGCGGTCCAAGTTTCACCCATCAGAGGCGCATTGTTTTCATCATCTG
AAAAAAAAATCTCTGTCTCTTAATAAAACACAAGAAAAAGTAGCCTTCGA
AAGAAAGCACATGAATGATATGTGCTGGCGACAGTGCTGGCGGCCTCTGA
GCCGTGGTGGGAGGTGGGAGCCAGCGGAGCCCCTGACCGATCACGTGACC
CACGTCTCTCCTGCACAGCTGGCTGCACCTGCACGCGGTGACACAGGGAC
CCAGCCTCCTGCCAGCAGGTCACCCCACCCCGTCCGTCTCCTGTCGGAGG
GGCAGCGTTGCCTTCTGAGGGTGGGCTGCTCTGAGGGGCGTCCTTTGGCC
Contig 77 (626 bp)
GCCATGGGCTGCGGCGGTTCACGCGGCTTGCCGGCCTGCCTGGAAGTCCC
ACAGGACCAAGGGGAGGGCACGTCAGCACAGGGGCCCCGGGCACGGACGG
TGCCGCCAGCCGCCCGGCCCCCGCCCTCCAGACAGGACGCCCGGTCACC
TTGCGGGGACAGCCAGCCTCGTGGCCTCGAGCAGAAGAAGTGAGAGTGGG
GTGCACAGGGGCCCCCGGGGAAGGAGAGGGGACAGCGGGGGTGAGCGGG
TGCGGCCGTGCTCGGGACCAGCCCCTGGCCTCTTGGCGCCTCCCTCCCCG
TCCTTAAACCGGGCCCAGCCTCTTGGGCCTCGACCCAAGGCTGTTTGGAA
AATAGGCTGGACCGTGGCCCTGACCCGAAGGCCAGCGGGGACCCGAGTGCG
GTCCCCAATGGATCAGCAGGCGCCTGGGCAGCCTGCGGCCCCGGGACCCG
GAGACACAGGTGGGAATGGGAGGAGGAGGAGGAAGACGGGAGGAGAGGAG
TGAGGACCAGCAGAAACCACGCCCTCCTCTCTTCCCGTCCTCGCCCTCGC
CTCCGACAGCTCCGACTCGGCTGCAAGGAAAAGGCCCCAGCCCAGCCCGC
CGCCACCGGGGGGGGGGGGGGGGGGGG
Contig 78 (500 bp)
TACTCGGGTTTGTTACCACTGAGCCACAAAGGGAGCTCCTAAAAATAATA
ATTTTCTTAAAGCCAATGACATGGAGAGCAGTTAGGGTGGAGGCTGGTGG
GTGGTGGGGCCGCGGCAGGCGCCCTGAAGGTCCTGAGTGGCACCCTTGGC
CGGGGGGAGGTGGGTGGGCGAGGGGTGTTGACAAGGGGCAGGGCCTCGTGG
GGGCAGGAAGGAAGAGCCAGTGGCTCCCAGTCCCCTGACCTTGCTGCCTT
GAGCCTGGTTCTCCCCAAAATTCTGTCTGTGTCCCTTCACTTCACGGAAG
CTTGGGGCCCGTTGCCAGGGAGACAGATGGGCTGGTGACACCCAAAATGA
GCCACCAGGAGGGGGGGCACTGACTTTAGCCAGCCGGTCACATCAAGAAGC
AAACAGGCCCCCCGCTGCTGTAAAGGCAGCTTGGGGCTGGGGTCGGGGAG
CACCCCCTGGGCTGGGGAAAGGGGGTCCTCTCAGGCCCCCGGGGAGGATG
Contig 79 (427 bp)
TCTATTCGCCGTGGCCGGAAGAGGCTAACCGTACATTGACCGGGCATCTG
GCGATGTATCACTTCTCTCCAACCGAAACTTCCCGGCAAAACTTGCTGCG
TGAAAACGTTGCGGATAGCCGAATCTTCATTACCGGTAATACAGTCATTG
ATGCACTGTTATGGGTGCGTGACCAGGTGATGAGCACCGACAAGCTGCGT
TCAGAACTGGCGGCAAATTACCCGTTTATCGACCCCGATAAAAAAGATGAT
TCTGGTGACCGGTCACAGGCGTGAGAGTTTCGGTCGTGGCTTTGAAGAAA
TCTGCCACGCGCTGGCAGACATCGCCACCACGCACCAGGACATCCAGATT
GTCTATCCGGTGCATCTCAACCCGAACGTCAGAGAACCGGTCAATCGCAT
TCTGGGGCATGTGAAAAATGTCATTCT
Contig 80 (650 bp)
GGCGTTGCCGTGAGCTGTGGTGCGGGTCACAGATGGGGGCTCAGATCCCGC
GTGGCTGTGGCTCTGGCCTAGGCCGGTGGCTGCAGCTCCGATTCGACCCC
TGGCCTGGGAGCCTCCATATGCTGCGGGAGCAGCCCTAAAAAAAAAAAAAA
AAAAAAGGAAGAAAAGAGAAGAAAGAAAAGAAAAGACAAAAGTCAAAAG
GAGCTCCCCTGAGCCGATGTCTGTCTACGAGCAGGTCCCTGGGAGCCTGAG
GCAGGGTGAGCCTGGACCCCTGAGGGCCACTCCAGACTCAGTGCTCTCAC
TGGCCAAGGTCTTTGGGGACCGGCTGGGGGCGCGCGCAGGCTAAGGAGGA
GGTCAGAGGAGGGGCTTCAGGCTGCAGGGCCAGCGGCAGCTCTGGGCCCG
GGGCGGGGGGGAGATGGCCTGAGGGCCTTGCGGGGGCTGGAGGGTGGGGG
GCTTCCTGGAGTGGGAAGACGGGAAGCCAGGTCAGAGGAGAGGAGCGAGG
GCTGAAGCTCCTGGAAGGCGCTGGCTACCCCCAGCTGGCCCGCCCCGCTG
CCACATTCAACAGCCACCCGGCCTGTGGTCCTGGCAGGGTCCTGGCAGAA
AAGCCCCAAGGGCCCCAGCCTGGCCCTCTGGGCCTAAAGAGCCAAGCCCC
Contig 81 (550 bp)
TTAACCCACGGAGCAAGGCTGGGGATCGAACCTGTAACCTCGTGGCTCCT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
CGTCGGATTCGTTAACCAGTGCGCCACGACGGGGACCCCCCAGGGCTGGC
GTTTCCCTCTGTGTGCACACAGTGGACCTGAGCCAACCAGCAGGGCCTTC
ACCACCACGGCGCAAGAGTCGGCAGCAAGAGAGCAGTGTCTCATGGCTCA
CTTTCTCCCCCTTCCCCGGAGTGGTGACAAAACCCGCCGCCACCGGACT
CGGTTAGACAAGGCGGTGCCCAGTGCCCCCGTCTGTCACCCGCACGGCAC
GGCGCTCTCCTTTCTTTCTCGGGGCTCCACCACGTGTCCTCAGTTTCCGC
ATGAGAGTACCGCGGCTGGCGGGGTGGTGGCTCTGGGGTCGGGGGCCGTG
AGGGCAGGGCTGGGCTGGGGGAGGCAGGTCTTGGCCCATTACGCGGGGGG
CAGACTCCACATCACACGCTCTCTGTGCCTCTTGGCTGCCTGACACCATG
GACTTCAAACAGGAACAGCCGTGGAGGCATTGCAGCCCAGGGCCCGGGTT
Contig 82 (550 bp)
TGACACCTCCAGGCAGGAGGGTGCAGGCTGGGGTCCCAGGTAATGGTGTG
CTGGCCTGTGGGGCGTGGGGCTCAGCTCTTAGGATGGTGGGCTGGGCGCCG
ACCCAGCAAGGACAGGGTGATGGCAGGTCGTGGGCTCAGCAAATGAGTGC
CCAGGTTGTGGGGGTGGGCACTTGGGGCTCAGGGGAAGCTCATCAGCTTG
GAGAGGGACGGGGGAGGGAGGGGGCCTTGGCCAGCTGGCCCAGATGCCTG
GATGTGAGCACTCACGTGCCCCGGGGTCCACCTCCCCTCCAGTGCCATCT
GGGCAGGAGGCTCCGATGCCTGTCCCTGGGACCCGCTGTCCTGAAATGAG
GTTCACTTGGTGCCTTCCCCAGAGATGCTCGGTCCGGAAGCTCACGAGGC
AGGAGTGCACAAGCGTCTGGGGAAATGGAGCAGAGTGCGGCTGGGGCACA
GAGGCTGCCCCCAGCCTGGGAAGATGGGGAGCTTTGCAGGGGTACCCCGC
CAGCTTCTGGGGCCCTGGATACCCAAGGGTGTGAAGAGGCTGAACAGCGA
Contig 83 (984 bp)
CTGAGCCCAGCTATGTAGATTAGACCCCGGTCCGTCCCAAATTCTTCTCA
AAGCTGTCCCGAGATGAGAGATGAGGTTTTCGTGTCCTGTGCTCTCCTCG
CTTCCCCTGGGATGTGCCCTAGGGTGGGAGAGGGTGTGTCCCAGGGCTCA
GCAGGCGGTCCCATCTTCCCGAGACGGGAGAGATCCCCTCCTTCTCGGCG
CCTGTCCCCACGGCCCCCACAGACACCCCCCCCCCCGGCATGGCACCCAT
GCACCTGCCATCGTGCCCAGTAGGGGATGGGTTTGGCGGAGACTGGAGATG
GCTGTAGCCAGTGAGACATGCCCTGCCACGTAGCCTGACCCCCTGGGTGT
GCTCTGTGAGATCTGGGGACCCCCAGCACACCTAGGGATCATCTTTGCCA
GCCTCCTGGGGAGCCTCTCAGAAATGGGGGCCCCCAGAAGGCTGGCAAAG
GTGATGGGGAGCGTGGGAAGTCTGGCGGTTGGCGGGGTGGGTGGGGGGCA
GTGCGGGCTGGGTGGGGGGTGCTCCGGGGTCGGAAGTGGTCCAGCAAGGT
TTTGGACACAAAGTCAGGAGGAAGGAGTGACGAGGAGACTTGCAGAATTA
CAGGTAGAATCAGGAACCCACATCGACGCCAATTGATCTATCCCCCCCTT
TGATTGTTTTCTCCTGGGGCTTTTTTCCNTTTTTTTTTTTTTTTTTTTTTT
TTAATCCCTCCTTAGCTTTTTACGCGCTCAACACCAAATTAAACGTACTC
CCCACCCCACGTAACAGGGGGGCGGTGACCCGAAGGACGAGGAGCACACG
AAGCCACCATCCGTCACCTTGGCGGCACCAGCCGCTGTCCTGCCCTCCGC
CCATTTATCGCCCTTGAATTGATTTTTGTTTTGCTCTGTCCCTGTCGCTT
GGGTAGAGTGGAAAAGGGAACCTCTGTGGGGGTGCCAGCCACTGGGCCCC
CCAAAGATTTCAGGGGAATGAAACGGCTGCCGCC
Contig 84 (550 bp)
TGCCCCTGACAACCCTGCCCTGTTAGCCACACTCGCGACTAATAAGGCGA
GAGGTCAGCGGGCAGCCCCACGGGGAGAAAGTGCCTCCGTGCCCCCCACC
CCTGGCTCTGATGGCCCAGCCTGGCACCCCAAGGTGGCCTCGGCCTTCCT
ACCTCCAAGGTCCAGGCGCATGTCCAAGCACCAGCAGAAGCTTCTCCAGG
GTTGGTGCCTGCTCAGGGCAGAAAGCAGGGGTGAGGCTCCCCAAAGGGCC
ACTGGCACCAATGCCCCCAGGCAGCCCCAGCGAAGGGGACAGCCCACCCC
CAGCCCGGGGACGCAGGCCTGAGGGGACATGGGGAACCCAGAGCAGGGCC
AAGGGGAGCAGAGCCCCTCCTCCGGGACTTGAAATCTTTCCCGGGGGGCC
CAGGGAGCTGGGGTCTGCAGAGGGCACTTTCAAAATACGGCCCACCCCCA
AATTGCCACGTGGGCCACAGAGCAAGGAGTCGCTGCCAAAGTGGCCTGGC
TTCAGCGCAGGAAGTTCCCCTCCTGGGGCCTCCCCTCCTATAGGCACAGG
Contig 85 (500 bp)
TGAGCCAGGGCCTGGCCCAGCTAAGCCCCTGGAGCCCTCCCGGCCTGTTT
CCTGCCTCCCATGCTGGCGGAGCTCGGCTTACTGAGCGGGGGGCCAGGCCA
GTGTGCGTGTGGAGGTAGATTCCACTCAGCTGGAGGTTGAGGTGGGCAGG
GGGCCGCAGACCCTCAGGCCAGCTCTGGCCGGCCAGGTCCCTGAAGCTCC
CCCGGCTGGCCTCCCCGTCCCTGCCTCTGGCCTTGTCCTGGCCCTTGCCT
GACAAGCTTCTGTGGCTCTGCCTGCAGGAGAGACACTGGCTCCCCGCTC
TCGGATGAGGACGGGGCTTTTCTGCACAAGTCCTGCCCCAGAATGTTTGG
GGCGCCAGCAGCTGAGCCCAGCACGTCTCCCCCCTGCCCCTGGCTGGACAC
```

FIGURE 6, CONTD.

```
GAATCCCGGCATCGAGGCGGGAAGGGGGATGGAGGGATGGGGCCTACCCA
CCCCTGCTCCCCACCCAGAATAGCTGGGCGGCCCCCATGGGAGGCCGCCC
Contig 86 (913 bp)
CTGTTTTCACGTCTTCTGAGGACACACCCAGAAGAGGGGCTGCAGGCGCC
CATGGTGACTCCATGTGTTCACTGCTGAGGCCTCTGCAGACCGTCTCCCG
CAGCAGCCGCACCCGTTTCCATGCCACCAACAGCGTGCGAGGCCGCACTG
TCCCCACGGCTGTGCAACTGTTTTGAATCTGAGTTATATAAGCAACAGAC
GCTCCTTCAAACACACTCACGTGCACACGTGCGCACAGGCGCACAGACAC
ACACACGGAGTAATAGGCCTCCCCCCCCTCCCTGAGCCCAGAGGGGGCCT
GGGGCCCTGGAGCCTGTGCTTTAGGGCCTTTTAGGAAAGCTGGTGCCTCC
CAGAGGGGCCGCCCCGAGCGTTGGCTTCCCAAGTCCCCACCAACCCTCGA
CAGACTCAAACGTTGGTTTCTTTCGTGCTTTTGCCCAAGGGATGGGCCCG
AGGTGGCCCTGCCTGAGGTTTCAGCCCAGCGCCCCAGGCACCCTTTCTCT
CCCGGTCCCCGGCCACTTCATGGGACAGCGGGCCTTCCCCCACGTTGTCC
CCTGGGTTGTCGTGCTTTTCGTAATGAGACGGAGGCAGCTGCACCTGTCC
TGGGGTGAATTCTCTTCTGCAGGAACTCGCTTCCCCGGCGCCTGGTCTGT
CTGTTCCTCGGTTGTTGGAACCTCTCGTCACCAGAAAGGGTGGCTCTGAC
GTCGCCCTTTCCCTCCGTGGCTTTTGCAGTCTGGGTCTTGTCGGGGAACC
TGCCCCAAAGAGGGGAGTGACCCCCCACGAGGGAGACGTAGCTCCTGTGG
CGACAGCACCGGGGGCCCCCAGATTCATGGGGTTCACGCTCACAGTCGCA
TGACGCTGCCTTTGGACGAGGGCAGCTCAAGGGAAGCTTCTTTCCTGCCA
CGAGCCACAGGCA


Contig 87 (650 bp)
TCCACACCTGTGGAGCCGCTGCCTCGCTGATGCCCTCTGCCCAGCTGATG
GTCAGGTGCCCAGACTTGGCGCTCAGTCCAAACAGGGCCCCACAGGTGCT
GCACCTGGGCAAGGGAGCCTGTGCGCAGGGCCTCAGGTGTCCCAGGCTCG
CTGGGACCGAAGCGCACTGGGTCCTGGACTCCGGGCTTCCCCAGGGGCTG
CTCGGGGCCACCTGGAAATGAAGCCCCACCTGGCTCATAGGGTCCACGTG
AGGGCCCTGAGGCCACCAAGCCACCAAACAACTCAGTTAAGGCAGGGGAG
CTTGGGGCTGCTAAGCTCCAAGCGGGAAGCGGCCGCACTCAGCACTGCCT
CTCTGCCAGCCAGCCGCCCAGCTTGCTGACGTCCCAACCAGGCCAGGGAC
CCTGTCCCACAGATGCTGGGCCCTTCCAGTCTCTGCTCCCTGGAGGCGCT
GGGCACTGTGTGGGCACACAGCCCGCACCCGCCTGTAAGGAAGGGAAAGG
CCCCATCCTCAAAAAAGCCGTGGGCAGGTGGGCCATCATGGTCCTCCCAG
GCAGGTCCTCCTGGGACCCCTTGCTCCCTCGGGCTCGCCCAGGAGCCGCC
AGGTCTGCCCTGGATTAACTCTGCCCCGCATGTCATTTTCAAACTGGCTT
Contig 88 (700 bp)
TGGGGCCCTTTGGGGCCGGAGCGCCCAGTCTGCTGGGCCCGGGAGCAGGG
GGTCTCTGTCCGCAGGGAGGGGGCCTGGTCTCAGGGGAGGAGAGGAGGCA
GGTCTCACCTGAAAGGATCTGCCTTCTCCTCAGGCCTCTGGGATGCCTGG
GCAGAGAAACCAGAAGGAAAGGCCCAACTTGCTGGCTGGTGCGGGATGGGG
CCGGGGGTCGCTCCCGGCACACCCCCCCAAACCCCACCTTAGTGGCCAA
AGTGGGTGTCATGATGGCCACTGACCTCACGGGGGGCGCAGGAGACAACAA
AATTTCAGCCACTCTTGGGGGAAGGACACTTGTGGCCTGAGTCTTAGGGG
CTGAGTTTCGGGGGGGGACCCCCAGCTCTCCCCCCAGTATCAGACACCCTG
CCCACTCCTCCCAGCTGCTCCCCAAACCCAGTGCTTCTGGACGGGCATCT
CCCCGCTGCCCCTGCAGCCGCTGTCCTCTGACCATGTCCCCTCCCCACCT
CCCCTCTGCAGGGCCAGGCCTCCAGGGAGCAGAGCCGAGGCCCCACCCTA
GACTGAGCTGGGGACCGAGACCCCAAGTCGCCACCCGGTCTCTGCGTTAG
AGAGGGGGTTCCGGGGGGGCACCCTGGGGCGGCACTGGGGGGCGGGAAGGA
GAGCCCTGGGCCGTTCTGGGAAAGGTCTGGGAGGGAGGGAGGGGGTTTTGC
Contig 89 (1400 bp)
GCACACCCGGAGAACAGAGGGAGGGGTCCTTACCAGTCTCAGGGTTTTTT
TGGGGATTTCTTTGAACTTGCCCTATTGGTTTCGAGGCTTCTGTTCTCTC
CAATCCCCCCTTCTGAACCCCCCCAAAAATGGGTTCAGCCCCCACCCCAG
CCAGAGGAAACCAATTGGGGGATTGGGGGGGAGGCGGGGCCAGCAAAAGCC
TTGGGCCCCCAGCCCCCCTGGCTTTGGCCTCTGGCCTGCCAGGTAGGGGG
AGGGACGCGGTGACCTCCGGGGGCCTGGCCACGGACTCTGCCCCTCACCCC
CAGGGCAGACGTGCACAGGAGCGGAGAGGCTCCGAGGAATGAGGCCATCA
AAGGGACAGGTGAGGCCACGAGCCGTGGGACCTGGAAGTGTTTAGGGCCT
GGGGGACGAGGCTGCCGCCTGCGGGCTCCGTGGTCAGGAGGCCCTCTGCC
CACTGAGCAGCTCCCACCACTGGCACACGAGCCTCTCTGGGGTCCGGCTG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
GTCTCCGGCAGGGGTGGGCTCTGAACGTCCAGCTCCGCAGACAAATCAGA
TTCCCCCGAGCCCTGAGAAAGCCCCCTCCCCCAGCCCGTCTCCCCACCTG
TCGGTGGACACGAGTGACCCCTGCTGACCCCCTGCCCGGGCTCCCGCAGGA
GATGTGAGAGAGTAAGAGGCGGTACAGGACGGCCGGGGCGGCCCGGGCGA
GGTGCAGGTGTGTGGGTGTGAGGCTGGGCACAGGCTGGCACAGCCTCCCT
GGCCCAGTCCCTTGGGCACCTCTGGGCACCTCGGTGTGCCTGCCTCCTGA
AGGGATCCACCCTCCAGCCACCTCCTCTCGGGCCAGCCCCCACCCCACCC
CCGAGCTACAGATGCCTGCGCATTCGCCCCAAGTGTCCTGGACCCTGGAG
CCAGGCAGCCCACCCGCTCAGCCTGGCCAGACCCAGCGTTGCCCTTCACG
CCCTCCTCCCTCCCGCCGGGTCCTCGCGCTCGTCTCCTCAGGTTGCAAGC
CCCTTCCCACCTGCCATCTTGCCTGCGCCCAGGATACACGGCTCAACTCA
AGGCCTCACTCCTCGCCCCTCTCCAAGGCTCTGTCCAGGCCCCTCTCTGAC
CTGGCACCACCTGCCGCCTCCTGGCAGCCCCAGCAAACCCCCTGCCACAG
TCCACGACAGTCCTCTTCTGGCTCTGCCCCCAGGATGCTTCTAGAACTGG
GGGGGGGGTCCTTCCAGCCCACGCAGCATCCACTGGGCCCTGGGCTCCCT
CCCCAGGTGCCCCTCAGAGCTTGCAGCTGGTGCAGACGGCTCTGCTCCGA
ACCCATGCTCCCTGCGCCCTTGGACCTGGTGAGATGTTCCAGGTCATTTG
GCTGCACCCAAAAGAGTGGCCCCTCAGGGTCCCCCCTGCGCCCCTCCATC
```


Contig 90 (350 bp)
```
GTACTGTAGGGCCTCATTCGAATAGCCTACTAGGTCACAGCTGATCCACA
CCTTAGGCCATCACAACTTCCCAGAGGTAGTGCCGCTCCTGTCGTTGAAC
AAGACGGTAGTGACTGCTGTGAGAGCTCAGATCTCGTGGGTCACTCACCG
AGTGTGGAACCCTGGGGGAAGGCTGTGGGGTGTCCCCGGCTGGGTGGCCA
TGTCATGTGCCCCTTTCTATCCCTTGGACGAGGCTGGTTCACTCGGCTCT
AGAGCCCCAAGCCCCAGCTGCTCTGCCAACCCCCCAAGCCTGAGCCTCAT
CAGACCCACCACCCCATCGCCATGGCTACGCAGGACACACCGCTCTCCAC
CCCCACCAGCCGCCCCACCTCCCCGAGGTTCCAAAGCTTGA
```
Contig 91 (1464 bp)
```
TCCAGGACCTGATGCAGCAGCCACGTCGCGAGCCCCCTCCCACGAGGCCC
CTTGTTGACCAGCGGCTAGGGAAGGGGCACCAGGGAGATGCTGAGAACGGGG
CCTTCCGAGGGGGGCAGGTGGGACTCACTGTGACCCAACACTCCCCACCCC
CCTCTCCCGCTCCAGAGGGTGCCAGCCTGGAAGCTGGCAAAGTCCAATCC
ACAGGTGGGCTCACGTGGGGAGGCTGGTGGCCCCCACCTCGTGGGGCCCC
AAGCTGCCTCTGGGCGGGGTGGGGGCTGCTCCCAGCAGGGTCCCATCCAG
CTTCTCCCTGGGGGAGACTCACAGTTCTGGGAGAAGGCTCCTGACTGCACC
GCAGCGCCCGCCCCCTCCCCAGACTCACCCAAGTTCTCTCTCTGCATCGG
TGACTGGTCTCCGCATTTGCCCAGGCTGGGCATCTGCCCAGAGGATACGT
CCAAAGGCAGGGCAAAGCCGGGCCCGTCCCCCGGAGCTCCCCACAGGCGC
TGAGGGCTGGGCTGGATCTCGGGGGGGGTGGAGGGGAGGACTCAGAAGGTG
CAGCGGGGTGGAGCGAGGCTGAGCCAAGGTGCACGCGAGGGCCACAGAAG
GCCGAGGCGGGCAGGAGGAGAGAGCGCCCAGCCTGGAGGGGGGTGGGTGCC
CTGGGCAGGTCTGGGGCTCAAGAAGAAGAGAGTGTGTGTGCCAGGGGGCTG
TCCAAGCTGCCCGGGAGGCTGCCTGCCCACCTCCAGGGAGCAAAGCAGGG
AGGCTGCAGCTGGCCCGGCCGGCCGCTCTCCAGGACCCACGCGTGGCCCAG
GCCCTCAACGCTCCTCCCCACAGCCCAGGAGACCCAGGGCACCGCGTCCATT
TACCGCGGGCTCCGGGTCCGTTTGCCTGCGCCCTGGGATGGACTGTGGGG
GCGGGGCGCTGTCTGGGGAGGAGGGAGGTGTCTGAGGCTGGACACCTTGA
AGGCAGGTGAGAGTGACAGGTCCGTGCGCAGCAGCCTTCGGCTCTGGATT
CTGGCCCTGAGCGAGGGGCTGGCTGGAAACTGGGCCGGGGCTGCCCCAGG
AGAGTGTGCAGGGAGAGGAGACGGGGTTTGGCCCCGGAGGTGCCGGGGGTG
GTGCCCTGGAGTGCGGCTGAGCGGGAAGTGGGTGTTGGCGTCTGGAGACG
GGGGGTCGTGGGCTTGGGATGGTGACAAGACCCCCCAGGTGGGAGGCGGCC
GCAGAGGAGGCAGAGAAGCCAGGCCCCAGCCCCACGGCGGGAGGCCTGGG
AGTCAGGAGGGACCAGCAGAGCCCTGGGCTCAGTGTCACCGGTCCTGGCA
CCTCGCCGACGGATGTCCTGGCCGTGCAGTGGTTGTCCCCTCACCCTGAG
CCCTGAGAACCATGCAGGATGCTGGTGTCACAGCAGGAGAGGGCCAGGGC
CTGGGGAGGAGTCTTACTGGAAGGCCTTCTCCTTCCGTTTGCAGCAGGCG
GGAATGACTGGGGG
```
Contig 92 (694 bp)
```
TGGAGCCAGGGCACGGCAGAGCGGTCCCGAGGCCGTGCGTGCTGACCCGG
GGGATGGGCGGACCTGGGGGTGGGCTGTGAGCCCAGGCATAGGGACCCCG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
ACTTGGGCACGGCCAGGTGGGGCCGGGCAAGGGGGAACAAGGACGCTGGC
CTCCAAGGGCCCCACGTGGGCACAGAGGAAGAGCCGACCCAGGTTGTGGG
CGCATGGAACCCCCCACTCTGGGGGCCAGGAGGCCGAACGTCCCAAGGGC
TGAGGCTGGGAGGGAAGAGTCCCTTTGGGGGTCAGTCAGTGTCCCTTGTG
GGTGCCCCCCTGCCACTGGCGGCACCTCTGACCCCAACTCCTTGCGGGTG
GACGGTGGATGGATTTCCTGCAGCCTTTCTTCTGGAATAGTCTCTGCCAT
CCTCCGGGGAAGCAGTGATTGCTCTGCCCAAGTCCAGGCCCCGCCCTGCAA
GGTGCCTCCCACCCCAATGAGCCCCCGGACAGTTCGAGGGCTTCTCACGC
TACTGAGGGGTATGAACAGCTGTCCCCCTCGGAAAGTGGGGGACAGGCCC
CTGCCACTCCATCCTCGGGACGCCCGGTCTAGTCAGCACTTGTCTCCCTG
CCTTGTGCCCCCCTGACCTTTTTTGAGGACCATCAAAACCTCAGCCTCTG
CCCCAGGAGGTCAAGCCCCCCGTCCCCCAGCCCCCAGACCAGCA
Contig 93 (900 bp)
CCAGCCCCATCCCCCGGCTGGTCCCCCACCACACAGAGCCCCCGTTTCCC
AGGGGACAGCACAGCCTGCCCCCAGGTCTTACATAAAGTCACCTTCTCAG
AGCTCCTGTCGCGGCTCAGGGGAATGAATCTGACCAGCATCCATGAGGAC
ACAGGTTTGATCCCAGGCCCCGCTCAGCAGGTTAAGGATCTGGCGTTGCC
GTGAGCTGTGGTGGAGGTCGCAAGACGTGGCTCAGATCTGGTGTGGCTGT
GACTGAGGTGGCGGCCAGCAGCTGCAGCTCTGATTGGACCCCTAGCCTGG
GAACCTCCATATGCCGCGGGTGCAGCCCTGAAAGGACAAAAATAAATAAA
TAAATAAAAGAAGTAAACACACCTTCTCTAGCCATAACCACCTGCCTAGG
GGCGGAGGGCCAGGAAGCGGCACCCCCCGCCCCAGGCTGCCCGTGCGCCC
CGGGCAGGCGGCTCAGCCTGCTTTTTGTCTGTGATGTGAGCCGCCCCAGC
CCCACATGCAGGGGCTGGGCTGCGCAGTAACTGCTTTAACTGACGGGAGC
TTCGACCAGCAATTCACCAGCGGGCATGCAGCCGGGAAGGGAAGTTATTC
GTGTGTAGCTATTAGGCGCCGGAGTGAGGGTGTGCCTCGCCCTGGGCCCA
CCCCTGGGGGGAGGCATCACAGGGGCTTTTGAACACCTGCCCATGAACACG
GGGCAAAAGCCAGCCAAGGGGGCAGGTGCCTGAGGCTGGGAACCAACCCG
TGTCTCTGAAATCCGGGGAATGCCCACTGCAGGCATGTTCAAAGGGTCAA
GACCGGGGCTCTGCCTGAGAAGGACTGGCGAAGGCCAACTACAAAAGCGC
ACCCCTCTGTGCAAACCCCCAACCAATGGAACAAAACTCCAGAGGGGCCA
Contig 94 (550 bp)
AGTCTCGGCTGTGTCCATGGGGTTGCCAAGGTGCCAGGCAGAGACCTTGG
GGACAAAGGTCCTGTGAGCAGAAGGACATGGCCACGTCCCCTGCTCAGCA
GGTGCCCAGGCTGGCGTCTGATGCCCTCGCTGGGGTGGGGGCGGGTTGAG
GGGCCAGGCCCAGACACCCTTCGTCCCTGCCGGAGTTGTTTGCCCTTCTG
TTCCTGGAAGGCCCCCCTGCAGGTACAGGAGGCCCCTGGGGCTGACGCTG
CACCTTCTGACACCTGTGGTCTTGGGGATGGGACAGGACAGGGAGACCCC
GGGGCTGGACGGAGCGGGTAAGACAGACAGTTGACTCTCTCCTCGAGTCT
GTGCAGGGCTCTCCCCGGCTTGGGCTTCGTCTGCAGGGCCTTTCGGGTCA
GGGTGGCCTCAAGGTGACGAAGACCTGGTCCTCGGGAGTCTGCAGGCGCA
AAAGTTGCAGCCCACCCCCCCGGGGAGGGGCGCGCCAAGGACAGGAGGGCC
CAGGGAAGTCTGGGGCCTGCAAGGCCGTCCGGGCTGGGGAAGGCCAAGGT
Contig 95 (1200 bp)
GTTTGCTCTCAGCAGGCAAGGGCCTCCGAGGCCTTAATAGCCCATAATGA
CAGCGCCCGCTCCTGGCATGGGGCCCCGCCTGGCATGGGGCAGGGCAGGG
CAGAGCAAGCAGCATGCAGCTTCTACCTTCTTCCTGACCTCGTGGCCCCT
TCCGAGGCCTCAGGGGGTCCCCCGAGTGGGACCCCAGCCCTGGCTCTCCT
CTCCAGAGCCAGGCCCAAGGCTGGGAGTGGCCCAGAGATGAGGGTGCCCG
AGCAGGGCACTGCCTTGGCGTCCCCATCCCTGGCGCCTCAGGGCCGTACT
GTCCAAAACCAAAGAAAGCAGTCAGCAAAACTTCTCCCAGCAAGCTGGG
GTCAAAGGTCGCTTCCGAGGCGTGATCAGGGTGGCCTTTGCTACTGTCAC
CGTGTGCCCTGGGAGAGGCACAGGGACACAGACACACACCTCCCGAGAACC
TGGGGCTTCCAGGGCGTCAGGCTGCCTGGGCCATCCCGGGCCCCTGTGGT
CCCAGGATCTGCCGGGACCGTGAGGGCCTGCGTCCCACCCTCTGCCTGGGA
CAGGCCCCACAGAGCTCACAGCCAGGGGACCGGGGACAGGGCCCCGCCTG
GGCCACCTGCCTCCAGCCTCACCCAGCCTGGGCCCCAGGCCTGTGCCTGC
GACACCCTGAGTCTCAGGACGGGCGCGGGACAAAGCCGCCCGGCCCCTCC
CCCGGCTGGGAGGAGACCCGCGTGGCCCTGACGTGTGGGCCTGTCAGAGC
TGAAATGTCACAGCAATTAGCCCTAACGAGGCCGAGGGAGGGAGCGGCGG
GGAGGCCGGCGGAGGGGATCCACGAGCCGAGGGCCCGGAGCTGGCCACCC
CACCGGTCGATTCCAGGCACTCAGGGATAATTCGGTGTTTAGAAGTCAGG
CGGCAGCAGAGAGCGGGCCAGGCGGGCTGTGCCCCCCCTCCCACCGCCCC
TTAACAGGTGCCCGAACACGCAGGTCTGGGGGAGATGCTGAGGTCGCCAAG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
GGCACCCCTGGCCGTGCCGCGGGTGCTATGCTGGTTCGGCACCATGGGAG
CTGCACCTGCAGCTGTATTGGTCTGTGTGTGTGTGTGTGTGTGCACGCGTGT
GCGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTACGTGG
GGGGGGGGGGGCAAGCCCGTGCGTGTGGTGCACAGTAGACATTTAGAAGGT
Contig 96 (600 bp)
GGGGACCAGGGCCCAGCCCTCCAGCTCCCACGCATACCTGCTAGGAGCTT
GCAACCTGCGAGAGCTTTGTGGACCCCCTGCCGGGTGACCCCTGAAGCTG
GCAGCTCTCCTTGGCTCTGCAGCGGCTCTCTACACTACCCCCTCTCCAGC
GGCCTCGGGCCCAGACATCACCCACCCGCAAGGGAAGCAGCAAGCATCCA
CCAGCTGGGCCCTTTTCCCCCAGCCTGTGACCGGCCCCGCGCCCCCTCAC
ACCTCTGCGGTCCAAGACCCCTCTCTGGCTGGGCCCTGGTGCTGCCCTTG
CCGTGCACATCTGGGGTCCATACCCCACCAACAGGCCCCACTTTTCTGTC
TCCCAGTGTCCCCCTCAGCTGCCCTGATGGGCCCACACCTGGCTTCTCTG
CTGCCCCCCTTGACCGCAAAAAGACTGGGGTCCAGGACCCCCTGCCCCAT
GACTGCCCTGGAAGACCTCAAGCCTCTCCTCTCAATCCTGACCCTTTAAG
GCTCTTGCCACGGAGAAAGCGGCTGGGGTTGGGGGAGGGTGTGGGTCCCA
AAGCAGCTTGCATACTTCTCCTGACTGGGAGCTCATTCCTCCACAGCGTG
Contig 97 (1350 bp)
CCCGCCTTATTTTTAAATTTCCGAAAACAAAAACCACACCTCTCCCGTCC
CCGAAATTATTTTCGTATAGTCTTATTCAAAGAAGTCCTGCCACTGAAGC
CCACTTGTCCTGTCCCGGGCTGCTTTGGCCAAGGGCCCTGACGGGCCCAG
GGTGGCTCATTCCCGCATCCCCGCAGAGGCCGCCTTCACATCCCATGCGG
GAGCCTGGCTTCCGGCACCCGGCTGTGCCCTCGCTGTGGCCATGGACTGC
TTTCGCAGAAGCATAGGGGCCACAACATGGGACAGCCTCGCTCTGCTCGC
TGTGGTTCCGCTGAACCTCTCAGCTGGACATCTGGGCAGCAAGCACCCCA
GCTTTGCTTCAGGCTCTGGTTCCAGGCTGGGCCCTCCTCGGCCCTGCCCG
CTGGGTGCCAAGCAGGGCTGGTCCGGCTGTGCCCCCGGGTCTATAGAAGC
CTCTGCAGGGCTTCCTACAGCCAGGCTGGGATTCGGCGGCTGCCCGGGAC
TGAGGCCCCCTCTGAGTCTGACCCCCCCCATCCTTCCCTCCCACACAGCCC
CCCGCCCCCGCTTCTGCTTCAGTGAGGCCCCACCCTGCCTCACTCGCTGA
CATTTCCAGAACAGGGGGTTCCAGGAAGCCCTGAGCCTGCAGGGGACTCA
GTGACCAGCCGCATCTGAATTTTCCCTCCTTCTGATCTCTGGACACACGT
CTGGCTCAGCCTGGCTCGAGTGCCCTGAGCTGGGGACCAGGACAGACCTG
CAGATGCAGGTCTGAGCCTGGGCAGGGCAGGGCCCAAGGCTCAGGGAGAA
ATTGCAGGTGTGAGATCAATGACCGGAGCCTGGATGGGGCCGCCCTGGCC
AGGGCAGCTTTCTCCCTGCAGCTCCCTGCCACTGTCCCCCCCAACTCTGG
GCTCCTGCTCTGGACCCAGTTGTGTGTTCCCCTCCTCCCAGCCGAGCCAC
CCTCCCCCATTCTGCCCCCCCCCAATCCAACACCCTATCGTGGGAACCAGT
GGAGCTGAAAGAAGGACCCCCCAAGGGCCCCCCAGCCGCTGTAATCCTTG
GGGGCCTCTGCCCAGGTGCCAGGTCTCGGGCAGGAGGGGCCGCGGGCACA
GCCGTGGCAGATGCGCCCCCCAACCCTGGGCTCGGAGGAGCCCCGCCCCC
ACTGACATTTCCAGGCCGCCCGCTGCAGACCCGGCTGGCCGTGATATTTA
GACAGGGCTTATTTGCCGTGACTGGTTTTTGATGACTTTGGGGCCCAGGA
TGAGCTCAGCCGAGCCCGCGTTGGCCCACCTTGGTCTCAGCTTGGGTTTG
ATAATATAACGCGTTCAACTGAACCGCTGACGCCTGCGTGGGCCGAGGCC
Contig 98 (1354 bp)
GCTTGCAGTAGTTCATCAGATTGGACGACTCATAAATGTCAAGACATCTA
AAGATTGGTGCATCCAATCATTTCCCACCAGGTTGTTTTTTTGTAGATGT
CAAGAAGCTGACCCAAAAACTCACGTGGAAATGCACGTCAACTGGGACAG
TTGAAACAATTTCTAAAAAGAAGAAGGACGTCCTGGGAGGACTCTTCGCG
CTCTTTGGTTTCGCTTCACTTTATATTATTAGTTACTGATTTTCCTAAAA
GCTGCAGTAGTCCAGACAGTGGGCCTCTATGAAGGGAGGGGCTCAGAGAT
GGTTGGGACAGAATAGAAAGCCCAGAAACGGCACCCCCGCAAATGTGGTCA
ATTGAGTTTGGGCAAGGATGTGAAAGCGGTTCAGTGGAGAAGAGTCTTTT
CAAGAAATCTCTGGTCCTGGATCCACTGCTCATCCAGGCCCAAGAGTGAA
CTTGGCGCACATTTCTCACAGTGTATACAAAAACTGACTCAAAATAATTC
ACATACCGTCGTGTAGCGTATGAAGCCATGAAACATCCAGAAGAAAATCT
CGGTAACCTCAGGGCATCTGGGGCCTCCACCCTCAGCACCACTGGCCTTG
GGGCCAGATACTTACGTGTTCTCCTGTGCACTGTGGGACGTGCAGCCAAA
CCCCAACAAGGTGACCATCAGAAATGTCTCCAGACGTCGCCAAATAACTG
CCAGAGAGCACAGGAGCCCCTCACTGAGAACCACAGGGTGGGGCAGAGAG
ATCTCAGACATGACACGATTAGGGGAAAACAATCTGACACACTGGCTTTG
TTAAATTTAAAACTTTTCCCCTGTAAAAGGCAATGGTAAGACATTAAGAG
GCGAAGTGGCAGACTGGGAGAAAATATTTGCAAATCATGTATCAGATACG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AAGAAGATGCAGGAAATCCTCAAAGTTCAGTCACAAGAAAACCCAATTCA
AAAACCAGCAGAGCAGACATACGATGGCAAATAACCACGAGAAAGTCAGC
ACCCGCTGTCCCTGGGGGGACGCGAGTCAAAGCCAGGAGGACACCAGGAT
ATGCCCACTGCCAAGGCTACGGATAACGGGAAGCAAGAGACACAGACAGA
AAGGATGCTTCGGTGCTGGGGAGGGTGGGGTGGGGCGGGGGGTCCCCCCC
TGGAGCAGGATGTGAAGGCACTTGGGGGGGGGCTCTGCACTCCTGGGGGCC
TTTGGCACAGGCGGAGGGCCCGGGAAGGCTCTAGGGGCACGGAGAGGGGT
GCCAGGCTTCCTTACCCAGCCCAGGCAGACCAGGCCCTGTCATGAAGCCT
GACGTGCAGCAGCAAGAGCAACATGCTACAGACATGTGTCTGTCTGTGTG
TGTG

Contig 99 (1000 bp)
GGTTCTCAGGCGCACGGGGCAGAGGCTGAGGGTCCGAGGGGCCTTTGGGTG
CTGGAAAGCCTGAGTTTGAATCCCAGCTCGGTTTCTTAAAGCTGTGTCTC
CACGGCCAAGGAATGGGGCCTCTCTGGGAAAGGTCTGGGGTGAGGCTGGC
GGGACCTGCCAGCCCCGGAGGGCATCTGACCAGACAGCTTCTCAAGCTCA
CAGGGCTTCATGGCAGGATGGGGAAGGCTGTGGTGGGGAGTGGGGAGCAC
TCGACACCCTGTCCAGGCCTCTTGAGTCACGGTGGCCTCTGAAAAGGGGT
TCTCTGTGTCCAATGAGCAAGTCTTTGTCCGGGGCAGGATTACTAAGTCC
AAGGGTGTCTGCCCCTCCGTGGGGCACAGAGCAGGGGCCCCAGATCACGT
GGCTGTAACTGCCAGGTTGCAAAGCCTGCCACCATGTCCCACTGGGTTCT
CCAGTTACCTTGGGAGGTGCAGGGTGGGGTGATGGGGAAACTGAGGCAGA
GAGCTGGCAAAAGAGTGCCGGCAGGGACTGCGGCCGCCAGACCCAGCTAA
CCGACCCTCACACGGAGCTGCTTCTACTTTGCAGCCTGGACGTGGGAAAA
GGTTACCCCACAGCAGCGTGTGCAGGCACGCTGGTATGTCTGTCTACTTA
TGCATATGTTCTACGTGCATGCACGTGAGTGTGCTGTGTGCATTGTGCCT
GTGTGTGTGTGCATGTGTGTGTGCACTCATGTGTCTATACGTGTGTGTAG
TGAATGCTTGTGCATGTGTATTTGCATGTGTATCTTTGTACGTGTGCAGT
GAATGCATGTGTGTGCAGTGGCGGCATGTGCGTGTGTGCGCATGTGTCTG
TTTATACCTGTGTGTAGTGAATGCATGTGCATGTGTGTGTTTACATGTGC
ACGTGAGAATGTGCACTCGTGCATGTTTGCATGTGAGTTTCATGTACACA
TGCTTTTAACGTGTGCACGTGTGCACATGTGTTTCTGTGTCCCTTGCACG
Contig 100 (1500 bp)
CGTATAAATATATTAATATAGAATAAAATAGATTGATAATATAGATAAAC
TAAACCCATTATCAATACCGGGTGGCCCCAGCAAAGGATACTAGCCAGTT
TATCAAGGTGCTAAGTCAGCACATAGAATGGCCACAAACGAAAACCTGTA
CTGCCTATGTCCACTCTAATGGAGTATGCCACTGACATCAGTGGTAGGTG
AGCTGAGTCCATCTGGGCTCCCAGTTCGGGCCCGGCTTGTCCCCCAACGG
AGGTTCCTTCCAGGGTTCCCCAAACCCAACCGGGCCCCCAGGTCTCCCTG
TCTTGACTCGTTTCTGGAGTCTTCTGGGGCTCTGCAGTCCTCCCTTGTTG
GGGCTTCTGTCCCCCTGCCCCTGGCCTTGCGGGCTCGGCCCTGCCCTGGG
TCCCGGGCCTGCGGGCTCACCCTCCTTCTTTCCCTGGAAGAGAGGGAGCC
AGGCTGGGCCGGGCCAGGAGGGAATGCGCCTGACTCTGCTCCAGATGGAC
AGGTCGGGACATGCAGTGGCCTCGCCTTGGGCTGCTGAGCCAAGAGCAGG
ACGGGTTCTTTCTGGAATCTCGGGCCAGCCAGGTTCAGCGTGTGGGTGGG
CAGCCGCCAGCATCTGTCAGGGCCGCTGCAGGCGCGGGGAATGACCTCGA
CTTCTGCTTGGCACCCAGCTCTGGAACAGCCCCCTGCGGAGCCTCCGCCC
AGAGCTGGGCCAGAGGGTCCCCTGTGCCGGGGACCCCAGCAGGGCCCCTC
CCTGACTCTCCAACCCACCTGCCTGGGACGGAGTGGCCCCCTGGCCTCCGT
GGATCTCTGGGTCGGGGCTCAGCCGGCTTGACAGCCTGGGAACAGCCAAT
GCACATCCCCAGGCCTGGCCACACCCTTCCACCGGGAGCGGGCGGATCTG
CATTTCGCCAGGCTCTGCGGGCAGCTCTGAGACCCCCGGGTCTCGGAGCC
CAGCCGTGGCCGTTGTACGCCCTGGGGGCTGTGGACAGCGTGTCCTCATT
GCCCCTCCGAGGTCCGGCCCAGGTCCCCTCCCACCTGCTCGCCCAGAGCC
CTCTCCCCACCAACCACACTTCCTGCTGTTCTGCAAGCGGGACACACACT
CCGGTTTCAGGACCTTTGCACGTGCCGCTTCCTCTGCAGAGAAATGCCTG
GAGCAGATGTTTGTCCGCACGGCTGCTCCGCGAGGCCTACCGAGAGCCCC
TCACCTAAACGGCCGGGCCTCAGCAGCCCGGGGCCCTGTCCCCACCGCCC
AGGTGGTGGGTTCTCCTGTGCCAGTGTGGGCATCTCTGTAAGATACCTGT
TTATCTGCTCATCGTCTGGTCTCCCCCAGAAGGTAGAGCAGGGCCCGGCA
CAGCCGTCCTCGGGGTGGCCACTCGCCCTTGGGGCTCAGCCTCCATGCAC
GGAGGGACGCCTGGTGACACGAGAGCCCCGTGTGAGTGTGCCGGGCCGCC
AGCCTGCCTTAGGTCACAGCCAAAGCCGGCATTAACCACCAGGCCCTCGA

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

Contig 101 (600 bp)
TCTAGAATACCTGGCCCTCCAGGGACGTGTCCTGTAGCTGCGGCTTTCAG
GGCAAAGTGTAATTAAACATCCCCAGGCTTCCCTTCCAGTTGGCACAGGG
CACCCACATGAGGAGCAGCCTCTGGGTGCCAAAGGGCCCACTGGTGCCAG
GCGCTGGGCTGAGTGCACCCCCGCATGCTTCCCGCCCACTCACCTGCTGG
CCCCACCCCTGACCACAGCACCTGTGGGAACACTAGGCCTGGCAGCCACA
CGCTGCTCTCACTGGGAGGCCAGTGCCAGGCAGCCTGCTTGGCTACGCTAG
CAGATGCCCGCTCGCCTCTGCCCCTGCCCCTAGCCCATGCAGGAGCCCAG
GGTGGGGCACAGGAAGGACGATTGGGGCCCCAGGTCAGGCACATCCAGGC
CACAGCCGTGGCCACACGAAGGCGGCCCTGAGGGGGCGTTGGGGGGCAGA
CCCTGCCCCCCCGCTGCCGCCCCAGCTCCAGGCATTAATTCCCAGGGACC
TGTTGCACTGGGTGGCCGCCAGCCTGCCCCCTTGCCTTCCAAGGCCTCTA
AAATGCCCCTCTTTTCGTAAACTAGGACTTACCAAGCTCAGCGAGCCCTC
Contig 102 (1867 bp)
AGTATATCGGGTGAGACTGGGGACCGGTCTGCCGGGAAGCCCCACCATAA
AGGCCACGTTGGGCCACAGTCCGGGCCACGTGAGTGTGGGCGGGTCCGCG
GGTCTGCTCTTGGAACACCAGGATCTCTAAGAGGTACCAGCCGAGGCCAA
GTTCACGTGAGCAAGTGAGCAAATGACTGAATGAGAGCCTGAGCGAATGA
GTGAGGGGTGAGTCCGTCCACCACGCAGCCTAGGCTCAGCCAACCGCTGT
CCCCGCGTCTCCACTGGTGACCAGAACGGAAAGAGTGGGGAAAGAGTGGT
TGTCTCCCACAACCCAGTCCCCAACCCCCCTGGACGCCCCACCCCTCCAG
GGGTGCCGGGCCTGGCCTGTGGGCCCCAGTCTGGAGGCTCTGGCACCTTC
CTCATCCGTTCTCCCAGCACCCCAGGTTCGTGCTGAGCCCTCCTGGCCCA
CAGGCCTCGGGGACAAAGAGGGCCACCTGGAGGCTCAGGGAGCCTCACCT
GCCTCGTGGTCCTGGCGGAGGCGGGTCTGGACATGTGATAGACCGGCCTG
GGCTCAGCAGCTCCTGCTGGAAGATGTCAGGGACAGCCTGGGCCACTCTC
CCACCAGGAGAACTTATTCCTCGGTGGGGTCCCCCCGGGGAAGGGATGGG
ATCCCAGCGGGGACCCCAGAGCGTCCAGCACACGGACCTGTCCCTCCAGC
CCCTGCCCCACACGGATGCTCACAGCTCAGCCTCGAACACGCACCTGTTG
GACTTTGCCTCCTGAGGCTGTCTTCTCAGCCGACGCGGGCCTCCGCTGCA
TGGTCTGGAAGCCCAGTGGGACTCGCTGGTGACAGGGAACAGGGGCTCTT
GGAGTGGGGTGCCGGGGGAGCCCCGAGGGAGCTGCTTGGGCCTTTGATGG
CTGAGTCGGCTGAAGTCAGGCAGGCTCCCCCAGGCTCCCTGACCCCCCC
CACCTCAAAAAATCCAGAGCATCCTTTGCTTTGGGTCTGGTGAGGCTCTC
TGAGGTCAGACCCTGCGTGGCTGGGCCAGTGGGGCTGGAGCAGGAAGAAA
GCAGGACAGCCCCGCCCCTGGCCCAGACTCCCCAAACCCAGCAGGAGAC
ACCTGAAACGGGATGGAACCATCCTGAAAGAGCCACCTCCTCCTCCTTA
TGCATCAGCTGCCGGGGTCTGGGGGCCCGCCCCAGGCCCCAGATGTCCGG
GCTGCTCCCGTCTCACATCCAGGGGTTTCTGGGCCCAGGACTCTGTCCCC
CCAAGCATGCAGAGGGTCCAGGCTGGGGTCTTCATGCCTGCCCGTGTGCA
TGGTGGGGAAGGAAGGGGACAGTCTGGAGACCCCCCGCCCTCCCCATGCG
TGGCGCCGGGGGACAAAGCCGGCTGGGGTCTCAGGTTTGGGTTCAGAGCA
AACGTTGATCTGACCTGGTTCTGAGATGCTCGGCCCGATGCTGCGTTGTC
CGCTCGCATTTTCCTGTTTTCTCTGGGAGGCGCTGCGTGCGCTGTGGCTT
CCGGCCAGCCCCACGGAGGGACGCAGGGTGGCTGGCGGGGTCTGGGGGCC
CCTGCCCGCACCAGAACGTCTGGCTCAGGTTTTTGTCCTCGTGACCCATC
ACTAAGGGCCACCCTCTGACCCGGAGCCCTGTCTCCGAGGTGGGAATTGG
GGGCTGTCCCTGGCGTCATAGGACCTGGTTGGGGGGCATCCAGCGGCTGTGT
CATGCCCCTCCCCAGAAGACTCTGGGGGGCTGCGGGAGGGTTTCCCCAGCT
TCGGGCCAGCCTGGGGAGGGCGGAAGGCGCTGCAGGGCCTTGCCTGTCCCA
GGGAGCATGGCTTCGCTGCAGACTGGGGCCCCGCACACCCAGCCACCACT
GGCCGTCTGGAAGCACT
Contig 103 (650 bp)
GTTGAGGATTCCTCGGCAATTTCCTCGTCACTGGCGCTCCAATCGCCTCG
ATGGGCTTCTCCTCCAGATACAGCTGCAGATCCTGGGCGGGCACACCGTT
GAGCGTCACCTCGTAGTGCAGATTGCACTCGTTGTCAATGGACATCCAGG
CCATGCCGACGGCATGTGGATTCTGTGCATCCGTGTGCTCCTGTCGCTTC
AGCAGAATGGGTTCCGCCGAGTCCCGAGCATCGGCCACTGGACGGGGCAC
TAGGCGGCCACGGATCAGGCTCGTCTCATGCTCGGTGGCCACATTAACGC
CCAGTTCGCCGGCATACAGCGACTCGAGGACCTTGGGACCCAACTTCTCC
ACACTACCAATGGCCTGGTTGAAGTTGAAGCTCGGCGTCAGATCCTCCAG
CTTGGCCTTCCGCTTGCCCTGCTCCTCAATCAAACTGATGTTGGGCCTAT
CCCGGGTGTTCACGTGCTCCGTTTCGATGTTGTAGGCCAGAGATCCATCG
GTGTTCAAGTAGACCCACGCCAAACCGCTGCTCTTGGTCGAGGATTCGGC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
ACTGTGCGGCGCCAGCAGGGTCTGGAAGATTTCGCAGCTGGCTCGGGTCA
CGATGTGTCCCTGGATGCGCAGATGTGGGTACTTCTTGGACTCCACGGTC
```

Contig 104 (1630 bp)
```
GGTGTTGTCACTGCTGTGGCTCAGACCCCTGCTGTGGCACAGGGTCCATC
CTTAGCCCAGAAACTTGCACATGCCACAGGTGCAGCCAAAAGAAAATTCT
TACTAATAAGTTGTTCATTTGCCTTTACGTAGAGTGGCATCAAACAGCAA
ATTTAAAACACCATCTATCAATACATAGACCGCGGTCAAAGGGAAAGAAC
TTTCTATTTCAGCACCTTTAACATGGCTTTGCCCGAATTTCGGGACCAGGG
TGCTGTGTTTTCATCTCTCCCTGCAGGTGGTCCCCAGATGACCAGGCCGG
TCCTGGGCGGGAGGAGCCGGACTGTGGATCCAGTTGCTTCCCAAGACAGG
CTGACAGGAGAGCAGCAAGGGCCACCCCCAACCGAAACCAAAGCCAGAAC
GAGCAGAAAGATGCCGTCTTCCAAGTGGCGGGCTGGGAGCTTCCTCCCATC
CTCCGGAGCCGTGAGGCTGCCCTGGAGCTGGCAGGAGCCACAGAGGACCC
GGCTTTGACCGCCCCTCTGGGACCCACAATCAGGACCCTGACTCAGATGC
TGAGGGGCCTGGACAACACCCCAGGACCCTGCTGCTTCCCCAGAACCGCT
GTGTCCATCAAGGTCCAGATGGCACCCGTGTCCCCACTGGAGCACGCACT
CCGTGGGGCAGGCTTTCCCTTGGGCACCGATGCACCTTGAGGGCAGAGAC
GGGGCCCAATAAACGTTTCCAAACCAGTGGGTGAGGGACCCGACCGGCCC
GACACCGCAGCCCGGATGCAGGGACTCCGTGCTTGCCCAGCCTCCCTTG
GGGTGGTCCTCTGTCCTCAGGGGTGGATAGGCCATCATGTGGGTGGCCTC
TGGGGACATCCGTTCTCTGATTGGGTGAGTTTCAGCCACAGAGATATTCC
CAGGACTACAAAGCTGGGTCCCTTGGGGCACCTGCTGTCACAAAAAGACA
AGGCCCTGACCCCCAGTAGCCAAGTTCCCCCAGGGGCTCCCCAGGGTCTG
GTCATCCAGACTGTGCCAGCCGTGCTGCCCGCCCCAGTCCTGCCTGACCC
GACTCTCTGTAAACATCCCCCGGCCCCACCCAGCTTTACCCCAAGGCCGA
AAGCACCAGCCCCCTGCACCACAGATGAGGCCCCATGGCTCCCCGACC
TAACTTCTGTCTGCAGTTGGCTTTCAGCCTCGGGTGGGGGCAAGGCCTGC
ATCTCAGGCTCCCGGGAGAAGTTGCTGCCTCCACAGCAGAGCCAGGGGCC
TGCTGACCACCTGGGGCCGGGTCGGATCTGGTCTAGAATGCTGCTAAGGTG
TCCTTGCAGGCAGCCCCGGGCGGCCCCGCCCTCCAGGAGGAAGGGGACA
TTGCCAGGACTCAGGAATGAAGCCATCCCAGGTTTTTGAATCCCCGGTCCC
ACCACCTTCCACCTCTGACCTCAGGCACCTCGGCTTTCAGAGCTGCCCTT
TCTGACTCTGGGACACGGGGCTGTGAGGCGCTCTCGGTGTGTGACAGCTG
GGGGGGGGGCACTCTCTAACGAGGGTGGGCGTGCCCAGGTGACTGACCACA
GCCCTTTCCTCTCTCAAAAAACGCCCGCCCGAGTGACCTCACCGGAGGCAG
GGCCAGGAACCCCAAACCAAACCAGAATCA
```

Contig 105 (1820 bp)
```
AGTGAGCCCTGCAGGACAGTCTGCTGAGGGGTGTCTGGGCTCCTCAGAGG
CTCATGGCCACGGGCACTGGGAGGATAGCAGGTGGACCCCTGCATCCAGG
TCCCAGGTCCCAGGTCCCAGACCCCCGGACAGGCTTTCTATCTGCAGGAC
GGGGGCTCCTGGGGCAGCAGGGATGTGGCTGTGAGGCCTCGTCAGTCTCC
CTGTTTCTATCTCTCTCTGTATCACACACACACACACACACACACACACA
CACACACACGCACGCACGCACGCACACACACAGAGGCGTGACCAGGGCTGCA
GACAGGGCCATGGGAGGACTGCCCGGCAGTGCACCCAGATGGCCACACGG
TGGGGCCCTCGTCCCACTTTTGCTGCTGATGCTTCCGCCCAGCTGCTGG
GAGCAAGCACTAGCTTCCCAGGGCTCTGACCAGAGAGGGATGGGAGCGGT
CATGGGTCAACAGGCGCCAGGGAATGGGGAATAGGATCTGAGGGGCGGGG
GCAAGGGGCCCAGGCGAGGCTGCACTGCCCAGAGCTCCCTGCACCTGCAG
GACCAGCCACAGGCCAACAGCTGCAGGCAGAGCAGGGCTGCTCCTGTCCC
CAGAAGCTGGCACAGCACATGGGGTCTGACAGCCCCACCCCGGGCCTCCC
ACAGAGGGGCGGGTCCCCCAAACTCCTCCCCCGTCCCACCTCACAGCTCA
GCATCTCCACTGCCTGAGGACGAGCCCAACACACGGGCACACACACACAT
GCACGCACACACATGAATGCACCTGCAAGCACACACTCACACGTAAGCAG
GTACACACATGCATGCACACAATGAACACACATGCACGCACACACGCATG
CACACACGCACACACACTCAAACACGTACATGCAAGCACATGCTGGTCCT
TTGTCCCCGTGGAGGGGAGGATGGAGGCCCAGCCCGTGGGGAGGGCATGT
GGAGTGTTGGGGGGCTGGCTCCAACGCCCTCGCTCAACAGGCACCAACGC
TGGACTGAGATAAGCCGGGGCGCTGGCTCCCTTGGGGCCGCTCAGCAGGT
TTGACGCCCACCACAGGTGGCACTGCCTCTTTCAGAAGACGGATGTGGCC
ATGCCACCCTCACAGCCTCACCAGTCCCCCCTCAGCTTTAGTGCTGTCCC
TGTCACTGTACCCGGGGCCTTCCTTCTTCCAGGGCCAAAAGCGAGTTCAG
GGGACAGTGGCGCCCCATAATTACTCACCCAGGGTGCTGTCCTCTGTGG
TGGCCTTGAGGCCAAGGTGCTCCCATGGGGGCCCACAGGGCTGGCAGGGT
CACTTCCTGAGAGCACCCAGGGCCAGGGGGTGGCCCAGGCCTGGCCGGT
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
CCCCATCTGGAATGAGGGCCTTGCGCAGAGGCGGTGCACCCCTCTTTACA
GCAGCCCCGGGGGAGAGTGACTCCTGCGTCATGGACCTGGGGGCTGACCT
GTCACGTGTCTCGCCCAGTTGCACCCCATCCATTTCCGGGTGGAAGGGAC
AAAGCCATCCTGGTCGTCTCAGAGGACCTCTGGAGCCTCTTGGCCCCAGC
AGCCCAGCCCCTCCCGGGCCCGCATCCTCTGCCCACCCAAAATCACCTGT
GCCCACAGGGTCCCCTTCTGGGTGTCCAGGGCGACCCAGAACTGCCCCTG
CAGACACACCCAGCCCAGGACATGGCCGCCTTGCCGGGCCTGTCTGCCTG
GGGCAGCCTGACTGCCACAGACAGGCCGCTTGGAGGACCATCTGCCTGAG
CCCCCAAGGCACATCCCACGGGGCCCACACAGCCAGCGCCTGTAGACGAT
GCCACTTGGGGTGGGGGGAG
Contig 106 (1500 bp)
TGCCGAATAGAGGTGGAAACCAAGACCCGAAAAAATGTCCACATTTTTCA
ATTATTAGAAATTTAGAAAAATATTTTACAGGAGTTAAAAGGTATTCCAT
TCTGGGGGCGGGTGGGCATGCCCACGGCATGCAGGCATTCCCCGACCAGC
GACTGAACTCGAGCCACGGCAGTCACCATGCTGGATCCTTAACCTGCTGA
GCCCCTGGGCAACTCCAGACACTCCATATTCATGTAAACTATTTTTTAAC
CAAAAAAATGACAAAGCTTTTCAAAACAAAACACATTTCATGGGAAGAGT
GGCATTGCTTCACGCCTGGATGGTCGCTGCGGCTTGCGGGACGACGAGGG
CCCCCGCGGGAGCGCCTCCGCACGGCGCATCAGGACGTGGTGTCCAGGGA
AGCGGGGTCACTTCACGGCCTCTCGGGTGCGCGTGGGTTTCCTTTTCGGC
ACCACACCCGGACTCAGCCACTTGGGGGTTCTTAAACGTGAGAGGCACTGC
GGGGCTCGAAGCCACATCACTGACCTCCTCAGACTCTGTTATGTGAAAAC
CCATCCGTCCACGAGACCAAAGAGACAGACGAACAAACGCAAGGTGCCGC
CTAGGTTGGGCACAGCATGAGGGCAGAGCGGAAACCTTGGCGAAATCCCG
GCGAAGCCTGGACGTCGCCAGCTCTTACTTGACGCAAACATAGGGGGATT
CAGGAACTCTCTTTACCGCATTTGCAATTAATTTGCTGCAAATCTAAAAT
CGTTCCAAGCACAATGCTCACTGCATGGAAAAACCCAGGGGTAGGTCTCC
CCCGATCAGGATGTTTCCCGTGCCCTCTGTGCGGGTGCTGCCCCCTGCG
CTGGTCAGTGAGAAGTGTCCCTCCACCGACGACATCAAACTTCCCAGGTC
CACGCTCTCTGCTGTCCTGGACGAAAACTCATCTCTGTGAATCTCCCGCC
AGCTCCGCGGGAGCCTTCCAGGGCTGGAAGGACGGCCGTCCCGTTCCAGG
GGGCAGGTGCACGCTTCCCAAAGCTCCGCGTCCTGCTAGGCACGCTCAGAC
GGCATCACCCACAAACCCCACGAACTGTTTCCCTCGAGGCGACAGGCTCG
CCCTTCTCCGAGAAAGCAGCCCGCACACGTCAGCAAGGGGCCAGCTGCGT
TTGTAACTCAAATGGCCACATAGAGTTTGTCCTGGAGGCACGGGGTCTGT
CTGGGCCGCACCACTGCACACGCACAATATGCTGGGACACGCTCCGGGGT
CCAGCTTCATGGAATTAATAAAGTTTACTGCTTCACCAAGTACATTCTTA
AGTGTAGCTGGCCGCCAGCCTGGGCGTCCGCTCCGAGGCTGCCTCTCTGC
CTGGAACCCTTGTGCTGGGGGACCCTCTCTCCAGCCCCACCCCAGCCCCG
AGCCCAGGCAACATCCTTCTTGTAAGACACCCGCTACCCTGCCCTCCCGC
TTCTCCTTCTCTGGATCCAATCTCCTCCGCTTCTAAGCTCTCTTGAGGCT
Contig 107 (550 bp)
ATGGCACTCGCGGTTGTGACTGAGCTACCGGACGGCGCGAGCAGGGCCAC
GAGGGCGACAAGCGCGGGGCTGAGAACCTGTGCGAGGGCAGGTCCCTGCG
GCTGCAGACAAGCCTCTATCGCAGGCCCACAGACAGGAGCCCCCGTGTGA
CCCTCAGGCTGCGAGACCAAAGTCACGGCTCTGCTGGGAAAACCTCGAAC
CTGATGACTGGGTGGGTGACCCCAGGACCTTGAATTCCGGCCTCTGCAGA
ACGCTCTGAGCCTACGGGAGTGGCCACCCTCTCGGTTAGGGCCTGTGTCC
TTCCCTGGCTTCCAGCCTAGAGCAAAAGCATTAAATCACAGTGTGGCCCA
GCCCGGACCGTGCAGGACCTTAGACAAAAGAGGAGGGGAGAGAGAGATGAG
GCAGAGAGGCAGAGAGACAGAGGTGGAGAGACAGATAGACAGAGACAGAG
GCAGAGAGAGAGACAGACAGACAGAGACAGAGGCGGAGAGACAGACAGAG
ACAGAGGTGGAGAGACAGGCAGACAGAGACAGAGGCCGAGAGAGAGACAG
Contig 108 (900 bp)
TTTCTAAACTCTCTTACTAGTTCTAGTTTTCTATTGTTTTCTGGGGGGGT
TCTATATAAACATTCGTGTCGTGATTGGAGATGGTTTTGTTTTTTCCTCT
CCAAACTGTATGCCATGTGTTTCTTTTTCTTGTCTTATCACACTGGCTAG
GACTTCCAGTAAAACACTAGATATGAACAATGAGAGGAGAGCCAGGCCTT
CTTCTCAGTCTTGGAGGAAACAGTCAGTCTTTCCTCATTTAGAATGAGAG
CTTTTCTTTTCTTTTCTTTCTTTCTTTTTTTTTTTTTTAATAGGTT
AAGGAACTTCTCTTGTATTCTTATTTTTTTAGAGTTGTTATTTTTTTTTT
CTCTCTTTTTAGGGCTGCACCCGAGGCATATGCGAGCTTCTAAGGCTGGGG
TCGAATTGGAGCTACAGTCGATGGCCTACGCCACAGCAATGTGAGATCTG
AGCCACATCTGCGACCTATACCACAGCTCACAGCAATGTCAGATGGTTAA
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
CCCACTGAACAAGGCCAGGGATTGAGCCCGCATCCTCATGGATGCCAGTC
AGTTTCGTGACCGCTGAGCCATGAAGGGAACTTCCAATAATGCACCAATT
TTAAATGAAAAAGACAAAGCATCCAGCCCACAGCCTGAGTAAGGAGTTTG
GAGGCCTGACCCCTGCGTGGTCCTGGGCCTGGGCCTGGGCTGGTCGGGGT
GGGGGGGGGTGGGGGGGACCCTGTGGACCCTCCCTCCTCAGCCAGGCCTG
CCCCTCCATCCCTAGCTGTCGGGGGCTCGGAGGAAGGCGGGTGGATGACG
GTCCCTGGGACCCCTCCTCATATGTATCTGGGTCCCTGGTCCCTCTGAGG
CCCAGGTCAGGTCATGGGAGTCAAAGGTCAGCCAAGGGGGTAGCCCAGAG
Contig  109 (950 bp).
TAACCCACTGACCGAGGCCAGGGATCAAACCTGCAACCTCATGCTTCCTA
GTCGGTTCGGTAACCACTGCGCCACAACGGGAACTCCTTTGCTTTTGTTT
TTAGGATTTCACATACACGTGATAACGTGCCGTATTTATCTTTCTCATCT
GAATTATTTCACTTAGCCTAAGCCCTTCAGGGTCCATCCATGGTGCTGGG
AGTGGCAGGATTTGCTTCTTTTTTTTTTTTTTTTGTGGCTGAAAATCAG
TCCAGGATTATCTTCTTTTTTCTGTTCATCTGTGGAGGACACAGGCTGCGT
.CCGTGTGACGCTCTGCCGGGAATACGGGGGCCGATCGCTTTCTGAGCCAG
TGTTCTCATTTTCTTGGGAGAAGTACCCGGAGTGGAACGGCTGGGTCGTC
CTGCAGTTCTGTGCTGCATTTTTTGAAGACGCTCGGAGCGCTTTCCACAG
TGGCTGCACCGACTGACATTCCCACCGAAGTGCACGGATTTCCCCATCCT
TTTTCCACGTTTTCCCCGCACTTGCTATTTTTGCCCTGTGGATGTCGGCC
TCTCCGTCAGGTGTGAGGGGAGTCTCCGTGCGGCCCAGGCGAGGAGCGAC
CGTGAGCGTCGTTTCACGTTCCTGTTGGGCCACCTGCGTGGCTTCTCCGG
AAAAAGGGCTGTTCAGGCTTCTTGCCCATTTCTCAGTCTGATTGTTTGGG
GGGTTTGCTGTTGAGTTGTGTGAGTTCCGCACGTATGGGGGGCATCAACC
CTTTATCAGCTATGCGATTGGCAAGTCCGTTCTCCCATGTTCCGCCGGCC
GCCTTGGCACGTGTGGGCGGTCTCCTTGGCTCTTCCTTGGTGCAGAAGGC
TTCGGTCTGATGTGGGCCCATTTGTTTATCTTCTTTTCTTTCCTCACCGT
TGTTTTGATGTCAGATGCAAAAATCCATTGCCAGGGTCTGTGCCGAGAAC
Contig 110 (306 bp)
CGCCACCTCAATCGCCGGTTTGTTCTGCAACACGGTCCAGATAACCAGCG
CACCTAACAGGTCGAACACTGCCAGAACTGCGAACAGCGGGCTGAAGCCG
ATGGTGTCAGCCAGTGCCACCGACAACCAGCGCAAACAGCGTACTTGCCAG
CCATGCGGACATCCCGGTTAAACCGTTTGCCGTTGCCACTTCGTTACGAC
CAAACACATCGGAAGAGAGCGTAATCAGCGCGCCAGACAGTGCCTGGTGG
GCAAAACCACCGATACACAGCAGCATAATTGCGACATACGGGTTGGTGAA
CAGGCC
Contig 111 (800 bp)
GTTTTCCATGATGCACCAGGGGGGCCGGGACCGCAGCAGGGAAGGCTCCA
TCCTGGCTCTGTAAGACCTTGAAAACACCTCATTCCTCTCGGTCTTGGCCT
GCTCTTCGGTACGCCAAGTTGCTGAGACTGATGTGGGGATCAGTGGGGAG
CAGGAATCTTTCTGATTCAGCCGTTTCAAAGTGTCCCAAGCAGAAGCTGT
GATGGCAATGCCAAGGCTATCCATGGAGGTGGCTGTGCCAGGGGCCCCAT
TTCCTGGGAGCCCATTCCAGGAAAGGAATCTTGTAGCCCCAGGCTCCAGC
AGCCAGTGCACGGCCCCTGGGACTATCCGGGTAGATCAGAGGGAGGAACA
GAGCTGTGGATGGTAAGCAGGTGGCCCAAGTCCAATTTATGTCTGTGGTC
CCAGCAGGGTGCCCAGGAGGCCCCTCGTAACTCTTAAGAATCTTGGTCTG
GTCAGCTAAATTGTATGACCATTGTACTGAGCACACATCCCGTTTAAGTA
GAATTTTCAAGGATGACTAGGAGTTTGCCACCTGAAGGCAGGAAGGGCAT
TCCAGGCAGAGGGTACAGAGGTGAGAGGGAGGCTCTGACACTTTGGGCGT
GCAGGGGGTTTGATGTGACTGCAGCTGGCACACAGTGTATGCCCAGGCCT
GGCACGGCTGTGTTGGTGTTTGGAGAGGAAGGGAGAGGTGAGTTGAGCCC
AAGGTCTTCCAGGCCAAAAGACTGAAGGTGACCGCGGCTGTCCGGGGCTG
GCCCGCAGACCAGGAGGGAGCAGGTGGGAGCTGGCTCTTGTTCCGGGGAC
Contig 112 (3062 bp)
.CACACCCCAGGAGAGGAAAGACCCACACAGTCCTGATGACAGCTTGGCTC
GGGGCTGGAGCCCCGAGTTATAAATGTCCATCACGAGCTGTGTTCTGTCA
GAGCCATCAGTGGGAAGGCCAGGCCAGCTCAGCAGCCCAAAAATGAAGAG
CTAGGTCTGGGATTGGGCCCAAGCAGAGGGCACAGGAAAGCCACATAAAC
AAGGCACCCAACCCCCCTGTCATCCACCAATGTCACATTCAGGTCACACC
CCTGGTCTTCGGGGGAGGTCCCCTAAGATCCGGTGGCAGGGGGAGGAAAA
GTCTGACTGGATTCCTTGACAGGTGTATCAGCGGAAGGCCAGGAGGAGTG
CTCGGGCACTGCCACCTCCCAGGGGCATGATGGTCATGGACCAGATGGCA
GTTATGGGAGGAACCTCCCCCGTGGTCAGAGCTCTGGGTGCTGTACCTGG
TCATGCATTTCGAGTGGAAGGAAAAGAAAACATACAACTCCACCCCCAGC
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
AGCTTTAGGCTGTTGGTCTAAAGGTCCTGCCTCCTGGAAGAGACACGCCT
CTGTCAGCGGACACTGCTAAACCTAAAGGAAGAACTGCCACCTGGTCACG
GGACTTCCTAGGCCAACCAACCTACAGGTGACGGCCCGGAGCATCACGAG
GAGGTAGGGGACGGGAAGGGATGCATTTGCTGCTCAGCGGATCCACTGGG
GCGTTTCTGGAGCCCCCACGCCCACACTTTACTGCAAATGCACAAGCCCC
AGGCAGCAGGACAAGTCACAGTAGCTCTGGGTTATCCAAGGAGTCAGGGA
CCTACCTGGAAGAGTCTAGAACAGGTGACAGAGGAGGGAGAGGATGGTAC
CAGCAGTATAGGGAGAATCAGAAATCTGACCCACCCTGGGGGCCTGACTG
ACTCCCAGACCAAATGCCACACTCAGGTTCCCCGTCTGCCTGCACTTCCA
GGGCTGGGCCACGGGAGTTATGGGCCCCAGGTAGCATCAGAGGCTCCCAG
GTACAGGCACAAGCAGCAACCACAGGAGGGATCCAGGCCAGGGAGCATCC
AAGAAGCAGCAGAAGCTCCACCTTAGGTACAGTTCTGGCACCTCCAAGTT
GAGAACATGTCCTAGACAGTGCCTGACCCCAACCCAATGGAGTGTCTGGG
ACTAGACTAGGCACGCCATTTTGGTCCCAGGTTGCCCCATCTGTACAAAG
GGTGTGCGGCCCCCAGGGGGACACAATGAGCTCCCATGGGAAGGGTCTTG
CGAATCTCCTTAGAAGCAGATGTAAGAGGTGACGTCCAGCTTGTGCCTGG
GATGTAGAAGTGGAAAAAGCACCCCTCCCCCCGACAAGGATGAAAGCAAGA
GGCACAAAACAACCTGAAATTCCCAACGCCCCTGGAGATCCTTGGAGAAC
TGGGATTCTCCACCTGTAGGGGCACCTGTGAGGAGAGGCTCTGTGAGCAC
CTGCTGACCTGGCACAGAGGATGCCCAATACTAAGAAGCATCAGCTAAAA
GTCTCCAGGAATTCCTGGAAGCTGAGGAAGGGCTCACGAGAGGGTACAGA
AGCCCTGGGGCTATAGATATAAGGGACGTGCACACCCACTTGCAGGTCCC
CATGGACCCCAGGGACATTCACAGTGATGGGCAAGATTCCCAAAATGCAC
CCCTTGTGTGTGGGCCTGGTTCCGTGGGTCAGCAGACACCACACCAAGG
CACAAAGCACACACCCTCAGGCTACTCTCCTCCCTCTCCCTTGTGGAACA
TGAGCCTTGAGATGCTGGGGCACGTGAAAAACACTGTCACACTTAGGTCC
TGGTGAAAACTGACTGCGGCCAGCGGAAAGAATCATAAAGACCCTACACC
CACACACAGCCTTAATTACAGCTGTCAGTGGGGCTGGAGCCCCAAGAATG
TCTACACCCATAAGACATAGCGTTAATCAGAAAAACAAGAACAGCCCCAA
CCCCACCACCAGGCTGACAACTAACAGGTCATGTTGGAATATCACTGGGA
ATGTTCTAGGAGTGTAGAAAGACACACCAACTAGGGCATGATGCAAAGAT
AATACTTCAGCCTGGGACTGGATGTGACACAGGGAAAAGCATAAAGTGAT
GGCAGAGGACTTTGATGTCAGTGATGGAAGCCACAAAAACTTCTAGCTTA
GCTCCATTCCCAACAAGATTGACTGCAAACCCCATGCTAAAACAACAGCA
AAAAGAAAGAATCCTCATTTCCAGGCATAAAATTTTTCCCCCAGTCTCTG
CTGTCCTCCATAAGATGTCTGATTTCAACAGGAATTACGAGCCTATAAGA
AAGGCAAGAAAAAACTACACACTGTCAAGAGAAAGCCATCAGAATAACCA
GACTCGTAGCACAGACACTGGAATTGTCAGGATATTTTAAATAACCGTGA
CAAATACATTAAAGATTCTAATGAGAAGGGGGTAGACATGTAAGATCACA
TAGATTTCAGCAAAGAGATGAAACTCGAAGGAAAATTAAATGGGAGCCCT
AGAGTGAAAAACACTGTAGCAGAGAAGATGGGTTCATCCGTAAACATGAC
ACAGCTTAGGAAAGAATCAGTGAACTTGAAGACAGGGCCACAGAAAATAT
CCAAACTGAAATGCAAGGAGGAAAAATAATGAAAGGGGGAGAGAGAAAAA
ATAAAAGAACAAAGCATCCAAGAGCTGGAGGGTGACACTGAAGAAGAGAG
CATAGGCATAGCTGGAATCTCAGAAAGAGAGAAAGAAATAACCCAAGATG
TAATGGATGAGAATTTCACAGAAGCGTTGTCAAGCAACAAACCATACATC
CAAGAAGCTCAGAGAACACCAAGCAAGGTAAGTACTGTAAAAAAATAGCC
CGAGGTATACCTCATTCAGGCTGCTGAAAATCCATGACAAAAGAAGTCTT
GAAAGTAGCCAGAAACAGAAGGCGTGTTCCATTCAGAGGGAAAAGACACC
ATTGTTGCCAGAAACCAAATAAACCAGGGCTGAAAGGGTAAAACTTTTTT
TTTTTTTTTTTTTTTTTGGCCATGCCTGTGGCATGTGGAGGTTTCCCGA
TCAGGGATCAAC
```

Contig 113 (1300 bp)
```
AAACGGATAAATACAGGTGACCCACAGGCAGAAGCTGAAGTACAAACAGT
TCACAACGGCACCCAAAAAATACCGAAGGCTCAAGGGTAAATCTGACCCC
AGATGAAAGGCCTTCTCACGGAAAATGGCAAAGTGGCGCTGAGAGGCATG
AGAGGTTCGAATAGATGGAGGGCTCCGCCGTTTTCCCGGGTCCGAGGATT
CAGTGACGTCACGACGCCAATTCCTCTGAAACGCCTCTCTAGGTTCAGTG
CAGCCCAGACCCACTGGCAGCCGCCCTCGCTGCAGAGACAGCCCAGCTGG
GTCTTGAGGTTCCTACAGCGAAGCAAAGGGTCTAGAAAAAGCCAGACGTCT
CTGGAAAGGGAGAAGCAGCCGATGGATTGGCATACGGCGACAGGAGATTC
CTCGGACAGTGGCACCAGGAGAGGGGTGGACAGAGACTGGTGCAACCGAG
CGGGCCCAGGAATAAGTCCACACCCACACGTACCATCTCGTTGTTTATTT
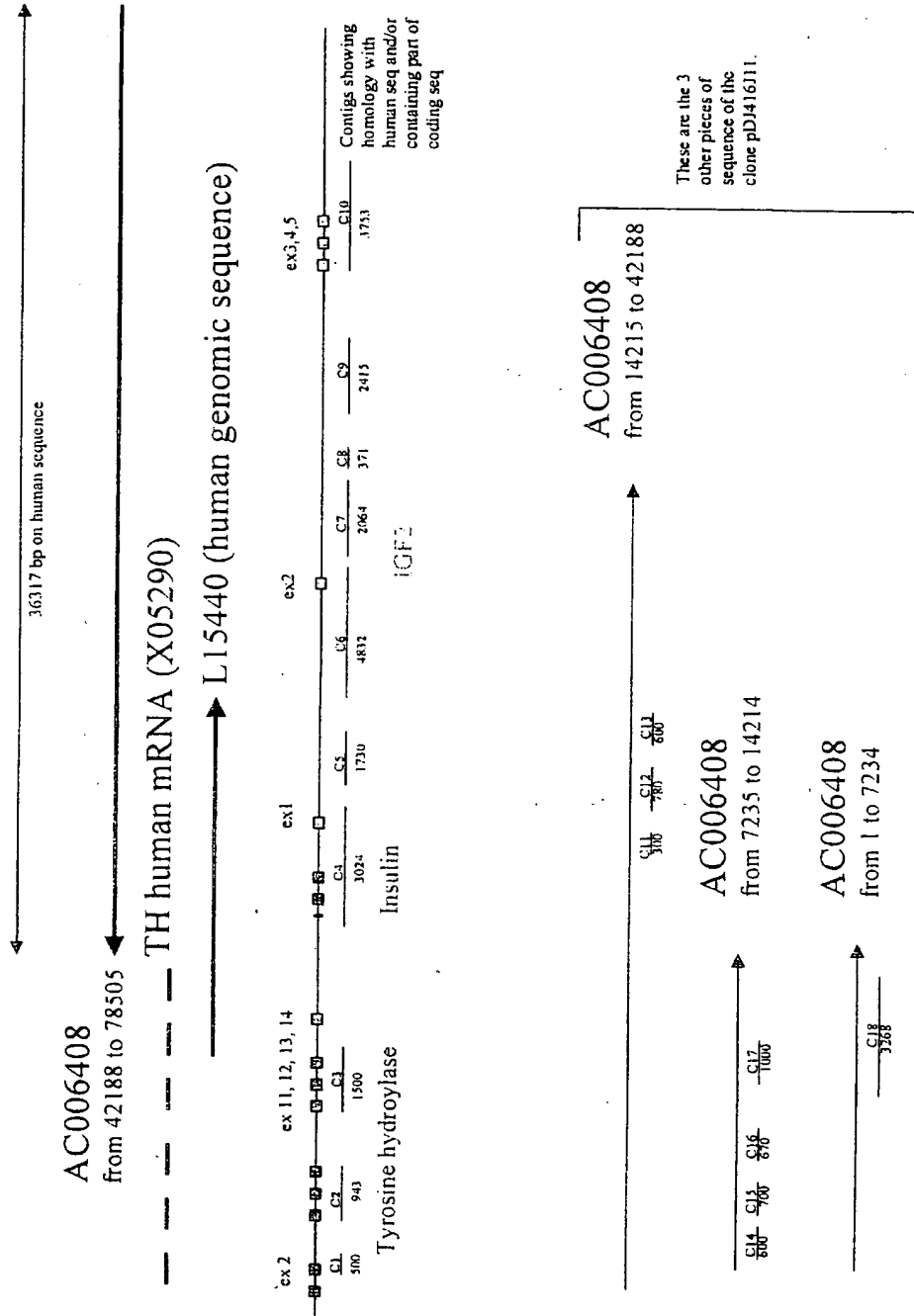ATTTTTTCCTTTTCAGGGCCACTCCTGGGGCATGTGGAGGCTCCCCAGCC
```

FIGURE 6, CONTD.

```
AGGAGTCGAATCGGAGCTGCAGCTACAAGCCTACCCCACAGCCACAGCGA
CACAGGATCTGAGCCATGTCTGCAGCCTACACCACAGCTCCCGGCAATAT
TGGATCCTTAACCCACTGAGCAAGGCCAGGGACTGAACCCACGTGCTCAT
GGATACTAGTTGGGTTTGTTACCACTGAGTCACAGTGGGAACTCCTTTAA
TTTTAATTTTTGAAGGTTCAGAACTCTTTAATTTTTTAGTGAGGTATAGA
TTATATTACGCACCATTTCTTTCTGACTTCGGTGCACGGCTTTTCAACAA
ATGGGTGCTGGACCTGCTGGGTGCCTTCTTCAAATGAACCACAAGCCCTC
CCTCGCGCCGTATGCAAAATTTAACTCGAGGGGCTCATAGACATAAACGT
AAACTCTAAAGCTATAAAATTTCCAGAAGAAAACGTAAGGAAAACCTTTG
GGGTCTTGGGCAAAGATTTCTTACCCATGACAGCAAAATTACAATCTACA
GAAGAACTGGTGGCCTTTATCGGCATTTAAAACACCTGCCCTTTGAATGA
TGCTGTCGCAAAACCGAACATGCAGCAAAACGGATGCAACTAGCAGGTCT
CACACTCAGTGACCCACGTCAGAAAGGGAAAGACACGCCACGTGACATCC
CTTAGATCCAGAATGTAAAACACGGCCCCCGTGAACCGACCTCAAGAGAG
AGACAGACCTACAGACGCAGCAAATTTGGGGTTGCCGAGGGGGATGCCGG
Contig 114 (3000 bp)
TGTGAGACCCCTTGGCGGGCCAGGACCCCCCAAGGTGACCGAAGGCCTCA
GCGCCCCCAGCCGCCCCATCCCCCTCTTTCCCGACACAGGATTTTTTTCC
CACCAAGCTCTGTTCCCTTGGTCACGCTCTCACTTGAGCAGCCTCAGGGT
CTCCCGGTGCCTGTATCCACGACAGCGTGACCTTCTTGGTGTGTCAACCC
AGGACCCCACGCTGGCCAGCCACGCCTTCCCAGAGCACCCCCGCCCATCC
TCAGAGTCCAGAGGAAAGGCCCCCATTGACCCCAGAAACCAAAACGCAGA
GACTCTGGGACGCCAGCAAGAACGTACACTGACTCCCACCTGCTTCAGGC
ACGGAGGCAGGGGTGGGTTATGAGCGACCCCGTGGAAGGGCCTTCTTGTC
CATCGAGGGGCTTCCAGGGGCTCCTAGACGGGGATGAGTGTGGCAACATG
TCGCCGCATTACAAAAGACCCTCCAGTGCTGCTGGGATGGGTCCCCCGGC
TAGAAAAGCAAAGGATTCCAGCCCAGTCGAGTAGGAGGCGGCCTCGGAGG
CTGCAGAGGCGCGGGGGGCGCTGACCACCACTCGGCAAGCCCCGTGTTGG
AGGGGACGCCCGGCCCGGCTGCAGCCGGTGCGCCTCCGGATAAGCTCCTA
AGAGGCCGCGTGCCCCATGCACGCGCGTGCACACACTCGCTGCCCGAGGG
TCCTTCAGCACAGACCTTCTGGGGACGGAGGACCTGGCAGGGGTGTGGCT
CTGGGGAAGGGGTCTGTCCCAGGAACCCTGTTCTGGATTTGGGGGTGGGC
GTGGATATCCCGTCCCAACCTACAGAAGGGAGGGGCTTAAAAAGAGCCCC
TTTGGTGTGAGGGGCCAGCAATCCTTTGGCTTTTTCTTGGCCCACTTGGA
GCTTGACGTCTGGTCAGTGACTGGGAGCCAGGGCCAGAGGGGGGCAGCCG
GGCTGAGGCAGGTTCAGGCCAACCATCTCTCGGCCACACTCCCGAGGTCG
GGCAGCTACGGGGCCCCCAGAGACACAAGCCCCAGGGGTCCTTCCCCCCC
GCCCCCTGCCCCAGATCACCAGGAGACCCAAGCAGCTCTGCCTCCCCGTG
CCTGAGAAATGCCCCATCTGGGTACCCAAATCACCCTCCCAGAAGGTAGA
GTGGGGGGCCCAGGACAGGGGGACCCCAGTTACAGAGCCCCAGGCAGGCT
TCCCAGGGGCGAGGGGACTCCGTTTGGGGCACAGACGGAGGCAGAGCGGG
CTGATGGATTCTCCCCCGGTTCAGGGATGCTGGCTGCCTGGCCTCCAGGA
GCCGGCGGTGCCATCTGATCTGATTAAGGCCTGCAGTCCCAGCTGGGCGG
GCACAGCCTGGGGGCTCGGCGGGCAGGGAAGAAGGCGCTGTCGCCCCAGC
CGGTCAGGCTCGCTTTCTCTTCATTTCCTCTCCATTAAAAGTGTCAGAAC
CATTTATTGATTTTTTAAATCAGGACGTGCTGTCCGTGACACAGCAAAGT
CAACAAAATCAGAGCAAAGAGAGGCCAGGGCTGAAGCCCCAGAGGGCGGC
GCCTCCAATCCGGTTGTGCCCCGGGGCTCCAAGCCCCTTCTTCTTCTGG
GGTCCTGGGCGTAGTGGCCAGGGCAGAATGCACCTGCCGTCATCCTGGGCA
GGCTTGGCCATCGCTGGCTTCTGTCTCATGACGCACCGTCGTTCCATATC
TACGGAAACAGCTTCGCATTAACAGGCAGGGGAGGCGGTTGTTTCTCCTT
TATCTGCCCACCATCGGCGCTGGGGCCACGTGGAGCCCAGCCGGCTGACT
TCCCGCTCGCACGCAGGGCACTGATTGCAGGAACGAGGACATCCAGCCCC
CGCCTCTCAATGCCCCGGGTGCTGAGAGCATTTCGCCCAAACGGCTTGGG
TGGGACAAGGGATGGAGCTGTGCGCCAGGGGCCTGGCTGGGGCAGAAGGG
GGCCTGCCCGTGTCTGCCCGTGGCCTCCAGCACCCTCGGCTGCCAGGCTG
CTCTGGAGAGGTGCCCGGGGGCCGAGGGCCAGGGGCACCCTGTTCTGCCC
CACGTCTCTCTGTCCTGCTGAAAGTTCCACCAGACGCGTGCTATACCCTG
GGAGTCAGGAGGATGGGGGATAGTTGGGGCTTGACGTCTGTTTCTGAAAA
AACACCGTTTTCCCTGAAATATATATGTATTAATTTTTCGTCAAGATAAA
ACTGTGTATAGTTTTTCGTGATGAGAAAACGCATCCATCTTCCTTAGAAA
GCCTGAAGAGGTACAGGAGCCTATAAAGGACAAGATGACAGATGCCTCTA
ACGCACACCAAATGTGCGGTGGCCCCCAGGGGACCGCATAGACGGGGCGG
CTCCAGATGGCCACCGTGTGCGAGGGACACGGTTCAGGGTGGCAGAGTAT
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

```
TCCTGGGGGGGGGGGGCTCAGCGGTTCCCATTTCCCCCTCCCTTCCTTCC
TTCATTTCTTTCCTTCTTTCTTTCTTTTTGTGGTTTTAGGGCCGCACCCG
CGGCGTGTGGAGGTTCCCAGCCTAGGGGTCTAATCAGAGCTACAGCTGCC
GGCCTCCACCACAGCTCACGGCAACGCCGGATCCTTAACCCACGGAGCGA
GACCAGGGATGGAACCTGGGACCTCATGGATCTTAGTTGGGTTTGTTCCC
GCTGAGCCACAACGGGAACTCCAGCCATTCCCATTTCTTGCTCCAGTTCC
AAGAATTCCAATTCTTATTCCTGTTCTTTAAGGCCAGAGGCGACAGCCAC
GCCGAGTCCCAGAAGCAGGGCTCAAGGATGCTGCTGTTGACTGTGTCCGT
GGGCGGGGGGAGTTGATAAGAACCCCCAACACAGGGTGGTGGCCAGCAAC
GGGGGAGGGAGGAGGGGGGGCTGGTGGGGAAAAGTCCCCTGAACCCCATGG
GCTGCCCCCTCCAGGCTGGGGCACGACCCCGAGCCCCATGGCCCGAGGAG
AAACGGTCCCAGCCCCAGGCTGGGCTCCCGCACCCCTGCCCTGACCCCGC
Contig 115 (1895 bp)
TCATGGAAGCCCTTATCACAACCTCGGATCCAAAACCCACTGCGCGAGTC
CAGGGATAGAACTCGCATCCCCACAGACCCTATGTTGGGGTCTTAACCAG
CTGAGCCACATGGAAACTGGGTAATCTATTTTTAGATGTTCCTAGGGTTT
TTGGCCTTGCCTGTACGTGGGGACGCTGCTGGGCCAGGGATCAAACCCGC
GCCACAGCTGTGACCCAAGCAGAGCAGTGACAGCACCGGATCCTTAAGCA
CGAGGCCAGCAGGGAGCCCCTGTGTTTAGATTTTGGTGAGGATACTGCGT
GGGATTCAGGATATTCACTTTGGGGCTGTTGGAATTGCCCGTCGCTGTTT
AAGCAAAGAGAAATCCCTTCACTCTGTGTAACTGTGGGGAAATCCTTTAG
TCTCTTGAAACCATTGCGTGTGTTTAAGAGTGGTAACTCTGCCACCATAA
ATGCCCAGACCAGCGCCTTCCTGAGATCCGCTTTTGTTGCAAATATCTGG
TTTGAATGCTTTGATCGCCCGCACCAGACCAGGGTGGGCGGACGCCGCCG
GGGACCCGACGTGACCATCGTGCTTCTGTATCCGCCCTTTCTCCGGCACG
CGCCCCCTGGTTGCCTCTGGCTGCTTTTAGTGGAGGAACTGAAGCCTCGC
CACCCAGACCCCGAGACCGCAGGACCCACAATGCTTCAAACACCTGCCCT
CTGACTTTTACAGGTCAAGTTCGCCAACGCCGAATTTGCACCGATTGGCT
ACAGAGAGCACGGTGGCGCCAAGCCTCCACTTGGAGTTTTATAAGGTCTC
CCTCCAGCTCGCAATGAAAATGAGCTGTGATAAGGCAAAGACAAAATTAG
TATGAAATCCAGATGCTTCATCTACAATACAATGACCGCGGGATTTGGGT
CTGAGCGACTGAAATCAAGGTGGGCTTCCGGAGGGAGGCTGTTAGAGGAA
AGGCATTCACGCAGGCTCAGGTCCGAGACGCTTCCACACCCCTAAGAGGG
CTGAGACGGCAAGTAGGGACCAAGCCCCGCAGTCGGGAGAGCTGGCAGG
AAGGAAGTCTGAGGTCACCCCCACCTGGGGAGGAACTGCCTAGAGAAGCG
GGGGCGGGAAGCAGGGGATGCCCAGTCCCAAGACAGGGACAGGGCGGAAA
GGGCTCTCTGCAGGCCCTCAATGCTGCCACAGTGTCCTCGTAAGAGGGAG
GCAGAGAGAATTGACACCGGGGAGACCACGGGACCACGGAGGTGGAGACC
GGGCTGCCCGCGCGTGCCAGTTGCTCCCGAAGCCGGCCCCTCCCCCAGAG
CCTTTGGGAAGAGGCGCCAACCTGCAGTTCTGCTACTCGGGGACAGGGAC
AGGGACAGCCCCCTGGAGCCGCCTCTTAGGGGCAGCATCCCCCAGAACCT
TCCTTAACAGACCATCTGGAGAGAGATGGGTCTGGGCTGCAGCTCCTGGA
ACTGTTTTGCCCACCCGGCGAGCACCAGTGGGTGCCAGCCTGGGCTGCCC
AGCCTCAGGGCCGGGGAGGGCTGAGGGCACTGGGGCCCGGCTCTGGGACT
CCCCTGCCTCCTGCCCGTGCAGGACAGCCACCTCCCAGCATCTGCTTCCT
GCCACCCACATCCCCAGGACCGTCAGCCCAGGCATGCCCCTGGCGTCGGC
CACTCACACCACAGGCCAGGAACCCAAGGGGGCAACACAGAAGGGCAGTT
GCCATCTGCAGATGGAATGGACAAACTGGGGTCCGTGATGATGGCAGGCT
CTGGGCGCCCGGGCTGGCAGGGGAGCCAGGACTGTGCGGCCATCACAGGA
AGGGCATGACGGGGTGAAAGCAAGAGTGGAAACCTCTGCCACCCGCCTGG
GCGCACATACCGGCCACCCTGCAGCCCCACCCCCATTTGTTTGCT
```

FIGURE 7

FIGURE 8

Contig 1   (1040 bp)

GCGCGCCGGATCCTTAATTAAGTCTGAGAGATCTGCGGCCGCGGCCAGGGTCTGCTTCTG
GCCAAGTGTGGGGCTCTGCTCCATCCTGGCTCGGAGGTCCACCCATGGCAAAGCCTGGGG
TCCTCCCACTGAATATTTGGGGGTCCACTCGTGCCAAAGGCTGGGTGTCCAGTGTGCCAA
CGGTACATGGAAGCAATGTCTTCCCAAGGACCGTCCAAGGTGTGGTCAGGCCTGGACAGC
TGTGAGTCCCTTCGGGACTAGACTTGGTGGCCGAACCCTAGGGACCGTGCCCGAGGGCCC
CCACGAGGCCAGGTGTTTGCCCCAGGGACAGAACGGCCAAGGGTGGCCGAGGGTTCTTTT
TGTTTGTTTTTTCTTCTTTCTCTTTTTCTTTGGCCGAGGGTTCTTAAAGCGCTCTCTCTG
CTCTTTGTCCCGATCCTGAGCGGGCAGTGTCCTGGTCGGTGGGGTGCTGGGCAGCCGCAG
CAGGGCTGAGAGAGCCCGGCTTGTCACTAGGGCGCCCGGTGAGCCCAGCGGGCATGCCG
TGTCCAGACGTTGGATGGGGCAGCGAGGGGACTGGGGTGCCCCAGCCCCCGTGGGAAGCC
CGCCCTGTGGAAGCCGCTGTGCTCGCCACAACAAGCACCGTCGACTAGCTGGTGAATCAG
CGCCCGTCGCCCGCGTAATCCCAGGCGCTTTCTGCCCAACCTGAGCCCTGACCCCACACC
CCTTGCGACCGCTCCGTGGACCCTGGGGCGATGAGGTGAACCGTGGGCTTGGCCATCGTG
GTGGCAGACGGTGGCACACCCGTGCGCCTGTCGGCCCCCCTCCATCCAGGAGCAGAGTGC
GCACCCAGTGGGGGCTGGGCAGGGAGCCGCCTCCACCTCCGCCCTGAGGGGACGGGACTC
TTTCGACCCGGAGTGGGAAGGGACATATGCGGACGATGCCAGACCCTGTCTGTGCGGGGA
GGGGGAGAAGGCCCTCTTTGGAGAATTCCAGGACGGGTGAGGAACGTCTGCTGGACCGGC
CGGGTCGGAGGTGGGCCTTG

Contig 2   (9234 bp)

GGCAACCAGGGGAAGATGGGGAAGCGGGGTGCAGGGGCGTTTGCGCGGGCCAAGGACCAC
CTTGGAAATCTGGAGCCTGGCAGGAGCGGCGCAGGGTTGAGGGGCTGGCTTGGGCAGGGC
TGGCTGGCACCTGGGAGCCTGGCGGGGTTGAGGTCCGGGGCTCCCAGGTGCCCTATAGGCA
GGGCAACATCGGCATGGGGGGTGACAGGCCCGAGCTGGGGTGCGGAGGGAAGAGGGGGGA
GCCAGGCATTCATCCCGGTCAATTTTGGTTTCAGGTCGTGGCGGCTGGTGGTCAGGGGGA
GTTGGAGAGAGGTTCGCCCCGGGGCCTGGGGCAGCGGAGGTGTAGCTGGCAGCTGTGGGC
AGGTGAGGACAGCCGTCTGCCGGGCCAGGTGAGTCCCCTTCCCTCCCCAGGCCTTGTTTC
TCTGGCCTCCTGCATCCGGAGGTTCTGGGGAGCGAGGGCCGGCGAGGCGAAGCGGCTGAC
CCCCCGGCAGAGTGGCGGCGGACGACAGGCAAGGCGGGCAGAACAGGTGACACGTCTCAG
GGGGAGCTGGGACCGGGCGGGGCTGGGGGGCCGGGGCCGTCCCAGGTGGAAAGAGCATCT
CAAGCGAGTCTGGTGGGAGACGAGGCAGGGCTGCCAGCAGGGAGGAGACGCAACAGGCGG
GGGGCATTCAGGCCCGGGTCGGACAGGACCCGTCGGGGGTGTCAGGACAGTGGGGTCCC
CAGCCGCCACTTCACCCACTGCAATTCATTTAGTAGCAGGTACAGGAGCGGCTCTGGCCG
GGCCTCTTGAGGCCTGAGCTGGAGCCTCGAGGGCCGGAGAATGGGAAAGAAGGTGCAGTG
TGCCAGACAGACGTCACCTGGAGGGAGCACGGCCGTGGGGACGGGCCCCAGAGAGATTTC
GGCAGCAGGGAGGCTGCGCGGGCCCAGCCTGCGGACGTGCGTTCCCACGCAGCACTGCGG
CCCAGGGGCTGGCGCGGCAGGCCCCCGGTGTCCTTGGTGGCACTGTGCGCCCTCGCCCGC
TCGCCCCTGGGACTGGCACGGCAGACAGGACAGCACCCAGGGGAGTCAAGGGCACTGACG
AGACCAGACTAGGCGAGGCGGGTGGGGTGGAATGGATGTGACCTCTGGGGGGAGGGAGGT
GGGGACGCAGGCAGGGGCGAGGCGCCGGAGCCTGGCGGCGAGCGAGGCCAAGGCGGGCCT
CTGCGGGTGACAACTGAGCACATATGGGTACCTTTGCGCTCGCACCGGAGACAGGTGAGT
GTCTGGCCCCGGCCTGCCGCCCTCCCGGCCCCGCCACTGCCTCTGCCCTCCCCCTCGACC
AGGGCCCTCTGCTTCCCCACAGCCTCGTCTCCAGTGGGGGTGGACACACTGCCAGCACCA
CAGGCCGGACGCCAGGATGTGCTTGGAGGGACATGACACAGTCCGGTGTGACGGAGAGGG
ACAGACGTGACGCCGTCCGGCCTTCCTGGTGAGCGCAGGTCCAGGCCTTGGCCCCCAGGC
CAGCCGCCCCACCCCCCACCCCTCATGGCCGTCTTCTGTCCCGCAGAACACTCTCGGCTG
GCCCCGCGGGGGAGCTGCCACACCCAGCGTCTGTTCCTTTGCCTTCCTGAAGGAGCACGT
GCATGACTGCTGCTCTCTGGACCCCAGAACCCTCAAACGACAAGGTGAGGCAGGTCCCGC
CTCGCCCCACACGTGGAAGGGGCGTGGGCGAGAGCCGGGCGCTCACGGTGCCCCCCTCCC
CCTGCAGAGATGGTGCTACCCAGCTCATGCCTGGGCCTTGGACCCGGACTTCTTCAAGTC
CTCCTAGCTCTGACTCAAGAATATGCTGCATTCTGGAGCCACTACACTACTTGACTCAGG

SUBSTITUTE SHEET (RULE 26)

FIGURE 8, CONTD.

```
AATCAGCTCTGGAAGGTGGGCGCGCGCTCCTCCCGCTCCCGGAGCCCCGCCCGCTGCCCG
CTCCCCGCTCACGTCCTGTCTCTGTCCTCGTCCGCAGGTTGAGCCAAAGGAACAGACGTC
CCACACCACCGGACCAACGGCACCCGCGGGGTTCCCCACCCCCCGCCCGGCCACTCCACC
TCGGCGGCCACCCCCTGCTGCGCCCTGGAGACACCACCAGCCTCCCTCTCTCCCCTTCCT
CCTTTTTTTCCTCTGTCTTTTCTCTTCTCTTCTTTCCTCTCCTTTGCTCAGAAGACTCGG
GGCATCCAGGACTCTGTGTCCCCGTCCTTCCTGAATTAATTTGCACTAAGTCGTTTGCAC
TGGTTTGGAGTCCTGGAACCAGCCCCGGGTCTCGGAGCGGGTGTGTGAGCTGCCGAGTGG
CCTGGCCTCCTCGGCCCGCGCCCCCTCAGCACCTGCCATTGTCCATCTCTGTCTGGGGGT
GACTGGGTGGGGGCCTGAGTGTGTGGGGCCCCGCCCTCCCCTCTCCTAGTCTGGAAGCTC
CGACCACCGAGCAGACCTCAAACGCTGCACTGAGTGTCCATCTCGTCATGTGCCCCTCCT
CGCCAGGGCCACCCCAGAGCCCTGGACTCATCAATAAACTCAGTTACCGGAATCTGTCTC
AGGGGCTTTGCAATTGGGCTGGGGGTGCGCCGGGCGAAGGGGGGGATGAGATGGGGAACAT
GCAAGGAAGGCCCTGTGGGCTGGGGGACACAGAATGGGTGGGGAGGGGGGCTCACAGGACT
CGGGGGGTAATGAACGTGGGGCTGGGCGCAAAGGGGAGTGGGACGTGGGGATCAGGGCGG
GGGGCCTGGAGGATGCAGGGTCCCTGCAGGGAAAGGGGGCCGAGGGCGTGAGGCATGTCC
TCAGCCCTGAGAGGCCCTACCCCACAAAGCACAGCCTGCGCGCGACCTCCAGGCCCCCAA
ACCCCCGCCCCAGACCCTCAAGCCCTGGTCCAGGGCAGTGGGTCTGACTGGCGGAAGGAA
CATGCCACCCAGGCTGGCCACACCACTGGGACGCCCATGGGCGGCCACTTTCATCAAGAG
CCTCGCCAGGCCCTGAGTGCTGGGCTGGAGGGCACAGAGGGTCCCCCTCCCCTCACGCTTT
GCGGTGCTGGGGCACCGCAGGAGTGCCCAACAGGAGACCCCAGGAAGTCTGCTGGGCTGC
AGCGAAGGGCAGGGTAGGGGGGCGGCCCACAGGGCCCAGCTCAGTAGGCAGGTGGCAGT
GGGAGGCGGCAGAAAGTTGGAAAGGGTGGACTGGGCACGTCAGGATCTCGTGGCGGCAGC
CCCGGAGCCACGGCCTTGGGTGCACTGCAGCCCCCACGGTTGGTGTCCCGGTCCCAGGCA
GCAGCTGGGCTGGTGACGCCCCTCTGCCTCTGCCCACCCCCCCCACCGCCCCCCCGCCAG
CCTCCCAGCCCCTGGGCGCCTGGCGTGACGCTGGGAACGCGAGGGAGCAGGCCTCGGAAA
CAGGGCTGGGTCCTTGACCCCTTCCTCTGCTCAGGGCAGTCAGGAAATGCCTAGCGGGCC
GACTGACCGAGAGGAGATAGCGGAGGCCTGGGAGACCCCGCGCTCGTGCCGTTCCCAGCG
TCCGGCCGCCGTGGCCCTTGGCTGGCCTGGTTTGGGCCCCATGAGCTCACCCCCCGCCCCC
CACAGCCTCCCCGCGTCTGGTCTCCTCTCTGGGCCCTGCTGTCCCTCCTGACGGTGGACA
GAGCCCTCCAGGGCCCCGGGGGGACGGTCCCGGGTCAGCAGGGCGGGTGGGCAGCACAGC
TGCCTTTGGTGAAGCCCCTGCCCAAAGCACCCTCAGCGTTTCCTCTGCGCGTCCGGCCGC
CCCCGGAGGCTTTCCCAAGTCCACGGGCAACTCGCAGGCGAGCCCACTCCACCTCCATCA
CGCGGGTTTGGCCAGCGGCAGAAGCACTCGCCCTTCAGGCGTCAGGAGTTAAGCCCCTCC
AAGGCCCCGTGCTAATCAGCTGCCTCTCCTGGAGCTTCGCAAAGCGGGCTCTCAGAGCCC
AGCTTCCCGGGGGCTCACCGTGGTGGCATGGGCACCACAGGTGGCCGGAGGGGCACCGAG
CACGACGGGGCTGTGGGGGGTGGAGGAGGGAGGTTCGTGACTCCGAACCTCTACTGAGGC
ACACAGAGGACACGGCCGCTTCCAGCGGGAGTCAGCCTGCGAAGGGCAGAGCGGGCTGTAGC
CTCCCGGTCACGCCCTCGCCTCTGCCCTGGATTCCTCCTGGGGGCCCGCGGCTCGTCGGG
GAGGTGAGTGCCCCTGGATGGGCGTAGGCTGGGGGGGCAGGGAGTGGGGGGAGCCCCGAGG
CCCTGGGCCCACAGCCCTGTCTTGCCCCACACACAGGGCTGTCTACACTCGGGTGCCCACT
TGCTCTGCTTCTAGGCTGTTCCCTGGGCAGCTGCCTGGAGGGCCGTGGGCACAGTGCGGG
CAGCCAGTGGGGAGGCCGGGGATGGGGCCGGGGATAGGGACCCCTGCCCCTGGGTGAGCC
CCACCTGGGCTGGGAAGACAGCAGCAGCGCCCCTTCAGGTCCATGGACCAGGGGACCCAG
GGTGGACTGTGTCTACCTTCAGCCCAGGCCAGTTTCCTGCTTGAGAAAGCCCGGGAGGGG
GTGCGGGACAGGCCCGGGCCCCCCACGCAAAGGCAGTTTCGGCAATGTCCCTGCGCTGACT
GAAATGTCACCAGGCACACGGCTTGAATTTCTCCCCCAGACCTGGCAGGGGCGGGGGTGG
GGGCACCGGGCTGCTGGGATCTTGGCCCCTGAACCTCCCCCGGCCCTGCGGCCAGGGAGG
GTTTAGGCTGAGTGACAGCCCACGGAAACCTGGACCCGACATGTCTGTGTGTCCATGTGT
GTCTGTGTGTGCGTCCACCTATGCGTCTGCGTGTGTGTCCATGTGTGTCCACATATCTGT
GTCCACGTGTCTGTGTCCACGTGTCTGTGTCCACGTGTGTGTCCACGTGTGTCCATGTGT
CTATGAGTCCTTGTGTGCATCTGTGTGCCCGTGTGTCTGTGTGTCTGTCCCCTGCAGTCC
CCGTGGACCTGTCTCTTATACACATCTCAACCTG
GCAGCGCCCCTTCAGGTCCATGGACCAGGGGACCCAGGGTGGACTGTGTTTACCTTCAGC
CCAGGCCAGTTTCCTGCTTGAGAAAGCCCGGGAGGGGGTGCGGGACAGGCCCGGGCCCCC
CACGCAAAGGCAGTTTCGCAATGTCCCTGCGCTGACTGAAATGTCACCAGGCACACGGCT
TGAATTTCTCCCCCAGACCTGGCAGGGGCGGGGGTGGGGGGCACCGGGCTGCTGGGATCTT
GGCCCCTGAACCTCCCCCGGCCCTGCGGCCAGGGAGGGGTTTAGGCTGAGTGACAGCCCAC
GGAAACCTGGACCCGACATGTCTGTGTGTCCATGTGTGTCTGTGTGTGCGTCCACCTATG
CGTCTGCGTGTGTGTCCATGTGTGTCCACATATCTGTGTCCACGTGTCTGTGTCCACGTG
TCTGTGTCCACGTGTGTGTCCACGTGTGTCCATGTGTCTATGTGTCCTTGTGTGTGCATCTG
TGTGCCCGTGTGTCTGTGTGTCTGTCCCCTGCAGTCCCCGTGGACCTGTGTGGTCTCTGG
TGTGCAGCCCTAGCCGCGGCCCGTCCCAGGCTGAGTGTCCCCAGGGTGCAGCACAGCTGT
GACGAGGGTGTGGGTCCCGCTGGCCGTGTCGCTGGGCTGTGGGCCCTATCCTCTTTGTGG
CTGCTCTGCAAGGCCTGATGGCTTTTGTGTGGCCTGGCCGTTCGGGTCCATGCCCCCTGG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 8, CONTD.

```
AAGAGCAACGTCTGAGCTAGCTCCACGCGTGGGTCCATCTCGGCCCAGGTTTAATGAGCC
ACTTTCAGGCAGGGATTGCACAGGAGGCAGGGTGGGAAGTGGCTCTGCTCAGACCCCTGA
ACAGGGTCTGGAGATTCTCCAAGGGCACAAAAGAACGGACGATGCCCCTGGGGTCAGCGA
CAATGCTCCCTGAGAAATCTTGGCACACAGGGCTGGGCCTGCGAGGTGGCCCCTCGCCCC
ACCCCAGCCTCCTGGAGGACAACCGTCGCCCTGCTCCCAGAGCTGGGGGGCGCCCACACGT
GGGGCACAGGGAGCATGGGCCCGATTCCAGGCCTGGGCTCCCTCTCGTGTCCAGGATCTC
CCCGTGTCTTGTCTCAACAAGCCCCTGACTTGGAGGCCCCAGGGTGACCCCTTAAAGGGG
GAACAGAAGGTTCTAGAAGGAGCGTGGCCAGCTTTGGCTTCCCTAGGGCTGTGGTGACCA
CACTGGGCCACGGCCCAGGCCACCCCACCCGCCTCCTTCCCCCTGGCCCCCTCCCTTCCC
CGCACCTCTCCCTGGCCTGCACCTGGTGACACGGCTGGCTCCCAGCCAGGGCTGAGGGGG
ACCAGCGGGGCCCCTTCCTGGAAGCCCACCTGCAGGCCGGCTTGCTGGGAAGGGGCCTGC
TCCTCGCCGGCCCCACCCGCCCGGGGCCGTTTCCTGGAAGCGGTCACTGGATATTTTGTT
CCTTGTCAGCGCCGAGCTTGCATAAAGCAGACACTGAGCTCCTTGTCCTCCGGGAGCACG
CGCTCCATCACCGAACACCTGGCCGGACACAGGCGGGCAGCCGGGCCTGGGGGAGCAGCG
CGGGCCTGGGGCCGGACCAGCAAACGATCACGGCGCCGAGCGCAGGGCCCGCGCCGCTTC
TGCAGGCCGCCCCCACGTGCCCAGGCCCAGCGGTGCCCATCCTGCAGGCTGGGAGGAGGC
TGTGGGCGCAGAGCTGAGAAGGGGGCAGAGGCACTGGGGGGGGACAGCCGTGTTCCCACA
CTTTGCAGAAACCTTGGCCGGCCTGGATGTCTTGCTGGGAGAGCTGGGGGAGGGGCACAGG
GCAGGAAGCCGGTCCCCCCGAGCGGGGTAGGAAGAGGCCTCGGCCCTGGGAGGAGGAGGA
GGGGAGGGCAGTGAGATGGAAAGAGCACCAGGGGCTCGAGGCTTCTTTCTGGAACAAGGA
CTAGAAGGAGGAGGCCGGGCAGCTGCTTGGGATGCTTGGAACAGGCCGGCCCCAGTGCTG
ACAGGGACGTGACCTGCCGGCCGGTCCCGGGCCCAGGCGGGCTGGGAGGGCGCCTGGTGG
GTCAGCGCCACTCAGAGCCCTGCCAGCAGGGGGCCTGGGCACGGCTGCAGGACAGAGCTC
AGGACACAGATGGGGGCGAGGACTGACTGGGGCACCACAGATGCTCCCAGGAGGTGGCCA
AGGAGTGGCCTTGGGATCCCAGGATGGCCCTGGTCCCAGAAGATGCGGCAGCCCAAGGGA
CCAGGCCAGGGCCGCAGGGGGGCCACAATCTGAGCAGGGCTCAGGCCCAGGGCAGAGGCCC
CCTCCCACCCAGCCCTCCCTGGGCCCGCCTCTCC
GTGCAGGCAGTGGGCTCAGATGGGGCAGACATGAGACCAGGTCCAGGGAGAAGCGCGCCC
CCTTGGCTTCATTCAGGTGGCTTTCAGACCGCGCCCCGTGCGTGGCAAGGCCCACAGCGC
TCAGGAGCACACAGACCCCCACCACGGGCTCCCCCAGGTTGGGCGGTGACATCAGCCCTG
TGTCAACAGCAGGAGCTGGCAGCTCCCCACCGGGGCTTAGGGAGCGGGGACCCTGAGCCA
CCCTGCCACCGCCCCACCCCACCGTGGCCCACACGAGGGCCCGCTGCTCTGGGTCTGGGG
CCAAGGCCCCCCAGGCGCCTGGCACTGTCTGCCCCTCCCGCTGGCTCTCCGTCTCCAGTG
TCCCCGCCAGAGAGCATGGGGGCCACAGGCCTGAATGCCACCCTCTTCCTCCCTCTGGAGG
GGGCCTGAGGTTTTGGGGGGTTCACAGAGTGCCCTCCGGGGTGGGTCCAGGCCCAGCGAGG
CAAAGCGGACCCCAGGGAGTCCCGCGGAATGTGGGACAGCCCCCCCGTAGATCTCCGGGG
GGCCAAGCTCTGGTTGACCTCCATCCTGGGGCTGTGGGCCTTTGGTCAGTGGGGAGGGTC
ATGACACCCAGCCCACCAGCTGGTGACAGCCCTGGACGTGCCGGCTCAGGGCTGGCCTGC
CCCTGCAGCCTTGAACCCCTGTTCTCTGGGAGTGGGGGCGCAGGGGGCGCCGGGGCAGGG
TGAGAGACGAGAGCCTCTCTTCCCAGAACTTCTGCCTGCGATGAGGACCCAGCAGGGGCC
TCTCCTCACCAGAGGGCCTCTGCCGGCTGCAGGGCCCCAGAGAGGCCCAGAGGCTGGAGG
CCGGGCCTTGGGAAGAGGCCGGACTTCCAGAAACCAGCTGCCCGCTCCGCAGCACCCAGC
GCCCACTTGGGAGGGGGGCGCGCCCCCGTGCCCCGCCCGGGTCCACTGCTGGGGCCGCCA
CAATAAAGTTTGTCCCTGCTGGTTACTGTCCGTGTCTGAAGGTTTCTGGAGCCTGGCCA
CAATGGGCGTCAGGATGCCGGCTGGGAGGGAGCCTCGCGAGTCAGAGTGTGCTGGTCTCGG
ACAGGCCCCGGCGCCCCCAGCCCGTGCTCTGTGGACAGATGGGTGGGTGGGTGGGTGTCG
GAGGGGGTTGGAGAGGGTGGGCGGGACGAGGGGCTTCCTGCACTCTGTCCCAGGGAAGCG
GGGACCAAGGAGGGGACAGCCCCCGGTCACCAGGAGGGTCCTGTCCCTCTCACCCCCCGG
GACAGGTGAGCTCCCCGGAGCCGCCCTTCTGGGACAGGACCCCACGGCCAGGCCACGGCC
CCCCCCACCCCGTGGTCCCTCCGTCCCACGGCCGGCCTGGGGGGGCCACGGGCCCAGGGCC
CCCGCTCCCCGTTGGCCCTCCGAGGGTGAACGACCTCGCCTGGGACGTGGGGCAGAGGGC
AGGCGCCAAGAGTGACCCCCTGGGACACGTGGCTGTTTGCAGTTCTGGAGGCAGCCGAGA
TAAAGCGGCTGTTTTCCCAGTGGGCTCAGGGCCAGAGGGGGGGCGAGGGGCAGCCCCAGTC
AAGGCCGGGCCGCTGCCTCGGGCTCCCCTCTGTGCGGAGGGAGGGGGCCGGTTGCACAGC
AGCCCCTGCCCGCCGCCCGCCCGCCGGCGCAGGCACCGTGGGACCCGGCCTGGTGCCCCT
CCCCCGCCCCTGCTCAGGGGCCAGCCCTCTCTGGTTCCCAGGACGCCCCCGCCCCGCAGG
CGGCCAGAGAGTCCCAGAGTGTTAGCCTCCCACGTGTGGGATCCTGTCATATGCGACAGC
TTAACTCAGGCCGAATTTCATGGGTCCTGGATTTGGGTGGGCACGGCCCCTGCACAGCGG
GGCTGGAAGCCTAAGGCGGTGGGCGTGGGGGTGAGAGGCCCGCAGACAACAGGAGGGAGG
CTGGGACACTTCAAGGGTTGACATGCTATGCCTGTCACGGATAAATGC
```

Contig 3 (5347 bp)

```
AGATGTGTATAAGAGACAGGGGCTGGGTGGGAAGGACAGAGGGTGGGGCCGGAGGAAATG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 8, CONTD.

```
GGATGCAGAGCCCACCGTGCACGCTCTGCTGGCCTTTGAGCCTCGCTGAGTCGCAAGAAG
CCCTCGGGCCTGGAAACAGACCCCCGGCCCCCACCCCCACCCCGGCCCCCGGATTACCCC
GGCATGGCTGGAGGGCCCGAGAAGCCACCCAGGCTTCCCGTGCCGAGCTGGGTGCTGGGC
CCAGCCGAGCGGGCTTGACGCCACGCTTAGCCCTCCCCAGGGAGCCCAGGGTCGGAAGGA
AGAGGCCGGCCGGAGGGCCGTGGCCGCTCAGGCTGGAGGGGGCCCCCGGGTCAGGATGGG
CCCCAGACGTCCCCGCTCCCCGGCCATCCGTCACGGAGCTGTCACCCAGGAACGTGCTCC
AGACGTGCTTTCCTCCCGCCGAGGCCCCGAGCAGGCTCCAGCCGCCCCCACCCCCGAACG
CCCACGCACACCCTCGGTCTGCGAACACCCTGCCGTCATCCGGTGGCCCCGGTTCCCGCC
GCCCGCGCCATCCGGGTGCCCCTTCCTCCCTGGGTCGGGGGCCATGCCCTCAGCGGGCAC
GCAGGCCTGTGCAGGTCTGTTCTGACTCTTCCCCAAAGACGCAGGCCGGCTGCGGGCGCC
CCGACCTCGTCTGAGGCCCGTTTGTGCTCACTGGCTGTCTCAGAAAGGGGTGCCCACGGG
AAGCGCGTGTTCCTTGGGCCGCAAGGCAAGGGAGCCCACCCCAAGGTGGCTGAGGGCAAA
TGGCCCAGGGCCTCTAAGGAGTCCCTGGGGGCCGGGCCGGCCTGCAGCTTGAGGAGGAGA
GCCCTGGCTCTGCTCCCCCGGGCAGGTGAGCCCACGGCAGGGGGCTCCCCAGCCAGCCTTG
GCAGGAAGCAGTGAGGAAGGGGTGAGGATGAAGGCAAGGGGGCCTGCGGGGGACTTGGGCA
AAGCCCCTGAAGAACTGAGTTCCTCGGAAAGGCCGGAGCCCTCAGCCGAGCCTCGGCCTC
CGAGCGATGGAGGCGGCCCACCTGCGGCCCCAGGGTGCAGCTGTGCATCCGTCCCCCTCG
GGCCTCCCCCTGCCCCCCCGGCCACCACACTCTCCCCCTTTTGCCTTTGATCACTTGAGT
GCGACAGCTTGTGCGGCCTGAGCCCCAGAGACCGCTGCCCCCCTGCCGCCAGCCCCACGG
GACCGTCCACCTGGGCCTGGCCTGGGCACTCATCCCTCCCGGATGAGGCCTTTCTAGCCT
GGGCCGCCCCGGGAGCGGCAGACCCAGCCCCTCGCCCCCCTCCCCCAGTGAAGGTGCTGC
CTGGTGGTCTGGGGAAGCCCCTGGAACAGGGGGCGCAGGTCCCACACGGGTGCTCTGGCC
TCCAGCTGCCAGGGAGGGCCGCGCTCAGGCCAGGGTCCCCTCCACCAGAACCGCCAGGGC
CCTGGGGAAAACCTGTCTGTGCTAACAGGGCCGCTCCCCGGGACTCCACGGAGAGGTGCG
AGGGACCCCTGAGCACCCACCGGCCACTAAGGGGCCCAGCCAGCTCGCGGGTGCAGGCAGC
CGGCTGGGCGCTCACATGCATACTGCTCTCTGGCTTTGTGTGTGCGCCTGGGTTGGGGTG
AGCGGAGGTGCCCGAAGGCGGAAGAGCCCACCCTCCACTCGGGGACCTATTTCAGCAAGA
AGACGGATGGGACTGCCGGGCATGGACAAAGGAACAGGATGAACCTTCTGGAACGCACAA
GGCTTCCACGGCTGACCGGTCATAGGAAGGCGCGTCTCTAGGCCAATCCACCGTCCACCG
TCCATTCCCCAGCCCTCGAGAGGGGGCAGGATGGACCGCTGCAGCGTGAGAGAGCTCTGG
GGCGCTCCCACAGGGCAAAGTCCCAGGGCACTGACCTCAGAGCCCAACCAGGCCACCGGG
GCTGGGCCCACCAGGGAGCCGGGGCCAGGGTCAGGGTCAGGGCCCAGAGTGCGGGAAAGG
GTGGCGTGTTGCTTGGGGCGGCGGGCGCGCAGACGGCCCCTCGCACCCCCCGACAGCCCT
GGAGCTGAGTGAAGCCCGCGGGTCACCTTGGCTGGGGTTGGGGTCTCCTGCGACCGGCAC
CCCAGCTCAGGTCATCCTTGCTGTACCGCAGAGGGGCAGGGGTTCTGAGCAGGGACAGGG
TGGGCCGCGCAGGAAGCCCCCTTCTCTCTGAGGCTGCCCCGGCCCTGGAGCCTCTCTGGG
GCATGCCACCCCTCTCACAGACGCCTCCCAGGAGCCCCCACTTTCCTGCTGCGTGGTCAG
GGTGTCTCTCACCCGATTCCTGGCCCCTGCAGGTCGAGTGAGTCCCTGCTAAGCCTGGGG
TTGGAGCAGGTGCAGGGCATCACCACACAGCAGCAGAGGCTGTGGGGGCCCCTGAGAGGC
GCTCCCAGGTACCCTCCTCAGGGGGCTGAGCCCGGGGTTGACCCGGGACCTCGCCTGCCC
CAAAGCCGGCGCCCTCCTCCCGCCCGCCCGACCAGGGCCAGAGAAGCAGGTGTGGGGCGG
CACAAACCCAAGTCAGCTTCCAGATCCTGCTGGGGCCGCGTTGAAACTCGAAGCCCCCAG
GCTGGGAGGTCTAGACACCCCTGCCCAGACCGACAGCCTGGGCCTGGCTCACAGCTGCCT
GGGGGCCCAGGGGTGCACCTGCCCTGTGGGTGGGGGTCAGAGGGCAGGGAACCCTCGGGA
AGGTCCCCCAGGGTCAAGGTTGGGCCTAAGCTCCGGTGACCTCTGGGAAGTCTGGGGCTG
GGTTTTGTTCCCAGAGGAGAGAGGGCCAGTAGCCTCAGAGGGGCTGTGGCACGGTGGGAA
GGCCCCAGGTGACCCCAGAGCGTGCGAAGCAAGCCCCCTTGACTGCAAAGC
GCAAAGGGCAGAGGTGGGGTGGGAGCCTCGACCCCCCGAGCCCAGGTACACAGGGGGAAG
GGCGAGGGATCCGGCAGGGGCCACACCCGCCACCCCAGGCAGCCCACAAAGCCTTTGGGC
CCGGAGCCCCAGATGGGCCCAGCCCAGCTCTGGGAACAGTCTTCCCAGAATTCCCCAGCT
CTGGGTACCAACAGGGCTGCCCGGCCCCCAGAGCCCTCGGGCGGGAGACCCTTCCCCAGG
GGGATCTCCTAAGTGGCAAGGCCTGTTGGGGAGGGGCTGGTGAGGAGGCCACTCTGGCGGGA
AGACCCCCAGCCACCTGGAGCCCCTAGCCACTGCCTGCTGCGGCTCCCTAGGGATCCAGG
GCCATCAGAGAAGCTCCAGCGACACTGTTTATTTTCAAATGACACTTTTTAAGAAAAACA
GCCTCACCCAAATGCTTGGCCCTGAGTCTGGAATGTGCAGACAGACAGCTGCCCCTCCCC
AGAGCCTGCACGGCCCTCCGGGTGGGGGAGGAGCAGGGGGCACCCCTGGGACCGGGCCGC
AGGCTGTCAGGGCACGGAACGTGTCTCTGGGCCCTGTCCTCAATTCCCGGTGCCCAGTGG
CCCCAACTTCCCAGCAGACCCAGCAGGGCCCCAGCTTGTCTTGGCCTGGCCGCTGGTCCT
GTCACCCCAGGCCTGGAGTTCTGGAAGATTCTGCTCCTGCTCCCGTGTGCACATACCACT
CCCCCGGGGCAGCCCTGCACTTCTGTTCCTGCTGGGCTCCCTGCCTGCATCCGTGAGGCCT
GCAGCCCGCCTGATCTTCCAGGTCCTCCTCCGAGCCCCCGCCTCCAGGAAGCCCTCCAGG
AGAGCTCAGGAGGGTCGGCTCCCTGCGCGCAGCTGTCAGACCCCTGGGCCCACCCCGCCG
GCTGCTAGGGTCCAGGTTCCCCACAAGCCCTCGGGCAGAGGCTGGGCCGCTGGGTCCCTC
GGAGACAACTGGCTCCGAGGCCTTGCCCTAGACGGGTTTCCGGGGAGCCCGTCCCCAGCGG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 8, CONTD.

```
CACCCACTGAGTTTTGAACACTTGGCGCCACCCCCACACCCCAGGCGGTGGCCAGGAGGC
CTCCTGGGCAGCAGACAGTCCGTGAGGTGGCCCTGGGGTGGCTCCTGACCTGGGCGCTGG
CCCAGCCCTGGGCACAGCTTTCCAGATCTTGCCTGCCGCTTCCTCCAGGCTGCCTCGGCC
CCTCCCGCCTGGGGGTGCCCAGCTTTTCCTGGAGGATGCCCACCCTTGCCCATGGTCAGG
GAGGGGCTGAGAAACCCCACCTCGTGCCTCTGCCCGGCCTATGCCAGGGGAACCAGGTTC
CCTCCCGCAGGAGGGGACCGAGTCCCTGACAGCCCACTGCAGAGGGGAGGAGGTGCCTGG
CTCTGCCCCCAGCCCCACCAACCCCGTGGCTTCCTGTTTCGCAGCCCACAAAGCACTAAA
GGCCGCAGGTCCTGGAACATCAAAGACCCGGGAAGTCCATTGTATTGAATTGAGTGTAAA
TGAGCCTGAGGCCTGTGGCTTGCGTTTCCCACAATTACCGCTGCCCGGGAAGGGCTCCGG
AACCGACACAGCCCCCAGGGCCCCTTGCCCATGTGGGGAGCCCAGGCTGGCCTGAAGAAG
CCCCATAAGGTGGACCCCACTTTGAGCCCCCACGAGAGTGGGCCAAGGACCAGGTCAGGG
GCTGCCCAGGCTCTGGGCCTCCTCTGCCTGCCAGGTGGGCTCCCTCGGGGCCCAGCCTGG
CCTGCAGGACCTTCCCACGCTGAGTTCCCCAGCCTGGTATGAGCGTAGTGGACGGCAGCC
ATGCCCAGCACTCAGGGGCCTGAGGGACAGAGCGGGAACTCCAGCCCCCGGGTCCTCGGC
CCCTAGGATCCTTCTAGGTGGGGAAGCCCAAGGGAGCAGAGGGGTGAACGCAGCTGTCTG
GGGCCCCAGGCTGCCGAGCAGACCCCTCCTGCTCCACTCCTCGGCCGAGTGGGCGCCGAG
ATGCCGGGGCAGTGCCATTTCCCAGGCGCCACCGGAGGCTCCCAGAGGGAGTGAGGCACG
AGCTCGGAGGGAGGGCGGGGGGGCTGGGGAGGCAGAGAGCGGAGGCCGGAGGCCGGTGAG
GAGGCCCGGAGCGGGGCCTGGAGTCAATGACCCAGGGATTATCGTGCTGGGTCTTTGCAAA
GTTGGCTGAGCAAACGCCGGAGCCAAGGGTCAGGGAGACGGGACTGGCGGGGGCCCCGCGG
CCCCCTTTCCCCTTTCTGGAAAAAGCCTGTTTCCCAGGTCAAAATCCAGCTCATGATCCG
CCCCCTTTGGGACTGATGTTCAGAGGCCCAGTCGGTCCCAGCACCTCTGTCCACCGCCCCC
CCCACGCTCCCGGGGCCGCCAACCCCTGTGGGCTGCGAGGTGCGGGCACCTCTCCCTTCG
AAGCAAAGCCCTGCCCTGCGTGGGCAGCGTGATTTCCTGCTTCTCTGGGGCTGCACTTTG
ACTGGGGTGGGGGGGTGC
```

Contig 4 (1592 bp)

```
AGCCCCTCAGCCCCTCCGAGCAGCTGCTGGGCTCAGCGGGCTCGCCCCCCGATGTGCGGC
CCTCCATAATCAATCATGGAGGGCCGGGCCCGGGGGGGGCGGGCCGACCTGTCAGCCAGC
TCCAAGGGCAGGGACAGCTGCTGTTCCGGAGGGTTCCCAGGGGCCAGCCCCACCAGACAG
CGGCCTCGGCCCCCCTTCCCCGAGGGGCACCCCCACGGAGGGCCCAGACCGGAGGGCACTC
GGGGCCCAGAGGCCAGGGCAAGAGTGAAGGCAGCGCCGGTGGGAGCGGCGGTCAGCGGGG
TCCAGGCTTCAGTTCCCAAGGAGCCCCATGCCCTGAGCCCGCACTGAGCCCTGTGCAGCC
TCTGGGTGCCGCCGAGGCCCGCCACCCCGCCCCCCACCAGCCTGGGGTCGAAGGAGGGAG
GGGGTGGCCTGACGGATGGTAACAGCTGCTCCCCCCACCTCGCCGGCGTGGACAGGGCTC
GCTTCTCCTGCCCGAGCCCCCGGCTGCCCCATCCGTCACGGCCCACCCCAGGACTGTGCGT
CCAGCCTCCCTCCCTCCTAATCCCCCCGCATTTTCCGAATTCTCGGGCCACTGCTGCTTC
CTCCTCAAATTCCTGGCCCCCCTCGCCCCATCCCCGCCATGGGAAAGGGCCGCGATGCCA
GGACACTTGCTCGTCTCGGCCGGGCGGGGGGAGGAGCAGCTGGCTGGGCCCGGCAGCTGT
GAGGTGCGGGGGTGCCAGGGGAGAAGGGCCCAGATTAGGGGGGCGTCATGGGAAAGCTGGGA
GGGAACGCTACCCAGAGCCCCTCCTGCCGCAGCCTGTGCTGCTCCCTCTCCGCATTTCTG
GCCTCTGAGTGCTCCCTGGAGGGAAGGGACCACTGTGTCCTGCCGGCCTCTGGCTCTGCC
AGGAATGTCCATCTGTCCGGGCCGGGTTACCTGGCTCAGAGCGTGGGTACCAGCTCATCC
AGCCCTGAGGCCTGCTCTCGGGAACAGTGGATGGGCCAGGCGCCCCCGTCACACCCCGCA
GCTGGGCTCCACAGACGGGCCCGGGATGGCCACGGAGGTGGGGGGCGGGCCCCAGGGCGAG
GCTCCCTCCTGGAAGGGCTAGAGTGTGGGCTGCGCGGAGAGGGAGGCCGGACGGCCAGGC
CAGGTGCAGCCCGGGGCAGGTGCTGGTGGGGGCTGTGACCCACGTGTGCAGCTCAAGGGT
CCAGGAGCCCCAGGGACAGAGCCTCAGGGACAGACCCTCAGAGCCACAGCAGGAAGCCTG
GTGGCAGTAGCTGGCGGGGCCGTGGGGTGCTCGGCCCTGCAGACAGAGGCAGAGGCAGGC
TCCCTGCTGATGACAGGGGCTTTCTCTGTCCCCTGGGGGGCGGAGGGGGCCCGACCATGG
ACCCCGGGCCTCCTCTCGCACGATTCCCAGGCCAGCCTGGTCTCAGGCAGTCCAAGGTTG
CACAATGGTCTCCATCGTCCAGAGTTGCAGAGCCAGCACTCTCCCACTGGACGGCGGCCC
GGGGTGGGCTGCACCGCCGCTCAGGGCTCAGGGCCGCGGCCGGCCAGCCCNCCGCAGGCC
TTGACCCTGTCTCTTATACACATCTCAACCCTG
```

Contig 5 (831 bp)

```
TGAGATGTGTATAAGACACAGGCCTTGACCCTGGGCCTGGCTCAGCTGCGCGCCCTCCTC
CTTGCAGCTCCGCCTCGACCCCATCCATCAGCCATTTTCCTACCCTTCCTGTAATAAAAA
ACCCGAAGCCGCGTGGCCCCGTGTCCGCTGGGGTGACTGCGGGCCTGCCTGCTGGTGGCTC
CCACCTGGGCCCGGCCCCCTGAAAACACACACCCGGCGATGGCTTGCCCGGGGCCCTGGT
GGAGGGGCGGGGGGGCCTCGCCTGCCTCTTGTCTGAAATTTTCGGTCCCACATGCCCCGAC
TCCTCTCCCGGCCCACCCTGCAGGCCCGGCCGGTGCCCCGGCCACTTTCCCGAAGGACGG
```

SUBSTITUTE SHEET (RULE 26)

FIGURE 8, CONTD. ;

```
ACTCAGCATTTCCCAGGGCACCTGCTGATGGTGCCCAGACCCCGGGGGCCTTCCCGCCGG
GCGCGGCCCCACGTCGCCCCTCCAGTGGCCACAGCGGGCCTGGGCCAAGGCTGGGAGTTC
TGCACGGGCCTGGGGGAGGAAGGCGGGGGAGAGGGGACAGTCTCCTGGCGGGGACGAGGG
TGGGGGCAGCAGGTGGGGAGTTCCCACAGCCGGGGCAGCGGGACGCCGCTTGGCTGCCCT
GGGTCTCAGCCCGGGACAGTGCCCACCAGGAGAGAGACGGCAGACAGTACAGCCCACCCG
TTTTATATCCTCTCAGGCGGTCTGTGCTTTATTGGGGTAAATATGCAGGACATAGAAACT
CTGCCACTGGACCCCTTGGCCGGGGGACACAGCAGCGGCATTGCATGCTTTCTGGGTGCA
GCGCAGCCAGCACCACCGGCCAGAGCACCCCATCTTCCCGATCAACCGGAC
```

Contig 6 (4634 bp)

```
CTCTGGGCTAGCACCGTGGGGGCTTTGCCAGAGTGGAACTGAACTGGGTCCACCCCGGAG
CCCAGAGGGCGGTGAATGGGAGGCAGAGCCCATCCTGGGAATGGACCAGAAGAAAGGGAG
CGGGGGTGGGGGAAGGGGCATCAGATCCTGGTCCTTCCTTGTCGCCTGCGGTCCCTCTGC
CACCACTCCCCGAAGCTGATCTGGAGCACACGCGTCGTTAAAGCCGCCATCGAGGCCCCA
CTTCTCACAGACGGAAGGGGGCAGAGTGCCTTCCTCACCGGCCTCGCCCTGGGAAGGCCC
CTCCCTGCAGCCCAGGAAGCCAGCAGCAGGTGACAGAGCCAGGGGCCCAGGGCCCCAGGG
ACGGGCTCGCGCGCCCGAGCCGGGGGTCCCTTGGCGTCCCCATCCTCTCGTCCTGGAGCC
CTCCTGGGTGACCACAGGAATGTGCAAGGCGGCAGCCGGGTGGCGGCCGGGAGGCGGGTG
GGAGGCGGGCGGGTGGCCTCTTCACGGGCGGGCCTGAGAGATGGGCGCCCGTCCGGCCC
TGGCGTCATCGTCTCCGCGTCTCTACCCACTGAGCAAAGACACACGAAATGAAGCTCGAA
CGAGCACAGCCAAAGAACGGCCGTTTCTGTCCTTTCTTCTTAATCCCTTTGGCTTAGGGT
TTCCCGGCCTGGACAGCCTGCCCAAGGGCACATGGGCATCCGTCCGGGGACATTCAGCCA
GTGACCAATCCCAGGCCACCCAGGCTGTGCCCTGCGTCGTGGGCCATTTCCCAGCCGGCC
AGAGATGGAGCAGCCACTGCGGGTCCCCGAGTCTCGGTGAGACAGTCAAGGATGGACCTT
GGATGGAGACCGGCGTGCGGCCATGTCCGTGGGTGAAGGAGGCGTGCAGGCCGTGCTCGG
GGACATCGTTGCTGTCCCCTCGGCCAAACCATGAAAAGCAGCCCTCTCCCCCAACCCCCA
GCACCAACCCGGAGACCACCCTCGGCCGGAGCCCAGCACGGCCACCGTCACGTCTCGGTC
GTCCAGCTTGGGACAGGTCAGTTCCCAGATGTCCAGGCTGGAGCTGGTCCTTGAAGATCC
TAGGGGTCCAGCCCAGCACAGGAGGGCCAGGTGAGAGCCCCCTGTCGGTTCTAAGGATGCA
ACCAGGGGCCGGCGGGGTGCCTGCCCTAGAGGGGGTAACTCGGCCCCCTGGGGACCCAGTC
ACCCCAGGAGGTCCCCAGAGCCCAGCTCGGAGGGGCCACAGGTGCCCAGAGTCCCACCTGG
GGAAGGCTGCCCCTCCTGCCAGCCCCCGAGCCGGGCCCCTGGCGCCCGCGTCCAGCCGCG
ACCCCGGGGAGATATTCACCCCCTGCCCCCGTGAATCAGGAGGCCCCGAGCCCATGTTTT
CAGTCCTTTTCCTCCCATCCCAGCCCCCCAGGAGAAGAGGTGCTGAACTGGGTCCCCTGC
AGGCTCCTGAGCCCCAGAACAGTGCCCTCTGAGCAGACGGGCACTCTCAGACCAGCTCAC
GCTGGACAAGTCAGCTCCTGCCTGCCGCCTGATGGGCCCTTGGGAGAAGCAGACATGGTG
AGGAAAAGGCCCCTGTGCCCTTCACCCTAATTCCCCAGCCCCAAGTCCCACTGGGTTGCC
AGCTTCAACCTAAGCAAATAATTCGTGCCCTCTAAACAAACGCGCGGGAATCCCACCTGC
CCTTCCCCCGCCCGCCCCCCC
ACCCCTGGCCTTGACCTCCAAAAGCACTTGAGGGGGGCTTTCTCCAGACACCCTCCAACCC
CGACCCCATGAAGAAGGGGTGATGGGGCTGTTACCCCAACAAGCAAGAGAACGAAGCCCA
GAGAGGAGTTGGCGTGGACAGCAGGGGTCAGGCCCCTTTGCCCCGAGGGCAGGGCTGGTG
CCACCTGGGTCAGGCGGCAGGCCCTGGAAAAGCACCGGAAATGAGCACACCTGGGTCTCT
AGAAGGTTCTTCCAGACCTCTGGGGGCTGAGTCATTTCAACACTCCTGGGCCGGGCAGGG
CTTCTTCTTGGCCCCGAGGGACAAGGTCCCCTTCGTCCGGGGGGTACGGCCCCTGGACCC
CTGTCCCCCGCACCCCACCCTCCGCCTGGTGAGGGCCGCGGCCAGCTCTGGACACAGATC
CCTCAGAGCCCCTTCTCCCTCCCTGCTCCCTCGTCTTCCCAAGATGCCCCGGCCTCCAGG
TGGGGCAGCCAGGCGGCAGAATGTGGTCCAGGCCTCTCGGCCCCACCCACACCCCCCTGC
TCTGCCCTGACAGCCTCCAAGACGCAGGCACCTCGCTGCGTTCTGCGTCCTGTCTCCTCA
TGGCACAAAACGGTGCCCGCCTAGCTTCCCCCAGAGAAGGGAGATCGTGCTCCCCGGACG
GACCCTGCTCTGCCTGTCCTCCCGCCCGGCCTTCAGGGCCTCTCCCCAAGGGTGGCCGCG
AGGAGGCCCTCGCCTCCGGCCACGGGGGCTCCATCCTCCCGAGCCCGACAGGCCTCCGCC
TGGTGGTCCGACCTCTTCCCCAAGGCCCCGCCCATCCTCCTCGCGCTCCCCCAAACCCTG
CCTCTTTCCCCAGCGCCCTTGTCCCCACGGAAGACCCTCCACCCGTGCCATTACACGCTC
TCGCCCCACCCTCCCAGCCACCCCCCCTTCCCCATCCTCCTGGAAGCTCCCACTTCCTTC
CCGTCTCCCACGGCAGCAGAGGGTCAGCAGCTCAGGGGTCCTGGGGCCGTGGAGATGGCC
TGCCCGGGGGTCTCGCTGACCGCCTCCTACGGAAGCTGTGCCGGGGGGTGGGGGTGTCTC
TGCCCGAACGGCTGGAGGACGAGCCACATCCCAGGGCAGCCGGAACCTGCGTCCTGGTCT
GAGACGGAGAGGCTGGGTGCAGGTGGCTGAGGGGCCTGCACACAGCTTGGCCTGGGGTCC
CCTAGGTGACAACACTGGCTGAACACTCATTGCTGCTCCCCTTCCAGGGTGACCCTGGGG
TCCCCGTGTGGCCCTCAGGGCACACGGGGGCCCCACCCAGGCCTCACAGAACCCCAGTGGG
ACTGCACCCAGGGCCCACAGAACTGCGGGGGCACTGGGGGTCCAGAAACAACCCCACAAC
```

FIGURE 8, CONTD.

```
CAGGCCAAGGTGGCCAAGGCCTTACTCGAGCGGGGCTGCCCGTCCCAAGAGACTCTGGCC
AGTCGTCCGGATCCAGCTTCCCGGGGCCGGGCCGCCCGCTGGGCTCCAGGCGGTTCTGGG
GGGCCCTCCCCCGGGGGTTCGCCCTCCGCTCTCAGCAGCAGGAAGAGGAGCGCGGCCAGC
GGATGGGGAGAAGAGGGCGCCCTGGCCATCTTGCTCCCCCTGGGACTTGAGGAGGGTCTC
GGGCCGGGCAGGCGGGACCGGGAGCCACAGAGACCCTGGAGGAGGCAGCATGGCGGGGAG
GTGACCGGGGAAGAGGGCCGTGTCCCAGGCTCACAGCCCGGCCTGGCCGCCCGGCCCTCG
GGAGGCGTGCCGCTGACCGCCTGGCCGGGAGGTTTGCTGCGTGTGGGGTTTGCAGAAAGT
GCTGAGCTGCTGAGCCCACAGGCCAGGCTCAGAGGGGACAGGAAGGAGGTTGCTGCCCAG
CCTCGGGCACTGCTGACCCATCTCCCGTTTCCAGGGCACCAGAGCCACCTAATCTGCCGG
CTCTGTGCCCAGGGACAGGCTTGCCTGATCTCTCAAGGCCGGGCGCTCCGCCTTCCCTGG
GAGAGGGTTAAACATCCAGCCCCAGCCAGCATCTCGGGCAGGTTCCTGGCTCCCCCCGCT
CGTGCCTCCTCTGAGACCCTGGTCGGCACACCTTTCCCTTGAGAGGAGGAGGAGGAGGAA
AGCGGATGGAACCAGTGACCCTGCAGCCCCTGAGGGCACCTTCCCACGTGCCCCCCGCCCG
CCCCGCGTCCTCCGCCCCCAGTTCTCACGGCCCCAGTCCTGATGGAGGGAGGGCGACCTC
CGGGCTCCCTGGCTCCCGCCGGCTCCGGAAGACAGGGCCGCTCGGCTGGGGCTGCAGGGA
GGGGCCCGAGACGCAGGAGAGCAGCCCGGAGGCAAACCCCGCGGGTCTTCCAGAAGGAGG
CCTGGCAGGGGGAGGGGGGTGCCACCACTGCTGTCCCTCTCGTGCCACAGTGGAGGGTGT
GGGTGGGCAGTGCCGGGGTGGGAAGTGCAGAAAGACCCTGGACCGTGGGGCTGGGCCGCC
ACGGGGGAGCGGGGTCTGTCAGGGACCCTGGGGGAGGGAGGCGAAGGGCTGGCGCAGAGG
CCGGATCACTTCCAGATTTGCTGTGGGACCAAGGGCCGGACCTCGGGGTGACTTCTTTTG
TGTGCTGGCCACAGGGGGGGCCCCGGCGAGCTCACACGGAAGGGGGCTTCGGACCTGGCCT
AACAAGCCCACTCCCGAGGAAGATGCAAGGGGAGGCAGACGGAAGGGCCGAAGGGGGCGA
TCGGGGGACACCGCGGCAGGGCCGGGGCAGAGAAGGGAGGCAGAGGGCAGAGAAGGGACC
CAGAGGGCAGAGAACGGAGGCAGAGGGGCCACATGCTTGGAGGGCCAGGGAGGAGCGGGA
ACGGCGTCCGGCGTCCAGCGCCGAATCAGGCCCGTCAGGCGGAGGGTGCGTGGACCTGCC
TGGCCTTCACGAGCACAGTCAGCAGGCTGTCTCTTATACACATCTCAACCATCAT
```

Contig 7 (482 bp)

```
AGCAATGGGGCCGTGACCTAAGGAGGCAGGCCCAGGTCAGTCGGGTGACCTCTCGTGGCC
CCGATGTTTGGAAATCCCCAAATCAAAATGACCCATCCGACAAGCTTGCATGCCTGCAGG
TCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGCCCTATAGTGAGTCGTATTAC
AATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTT
AATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACC
GATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTT
CTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCTCAGTACAATCTGC
TCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGAACCCC
TT
```

FIGURE 9

Human clone af087017.em_huml: H19 gene + flanking sequences

SUBSTITUTE SHEET (RULE 26)

FIGURE 10

IDENTIFIED POLYMORPHISMS:

POLYMORPHISMS TYROSINE HYDROXYLASE GENE - CONTIG C3 (figure 6)

1	GGATCCAGCC(A:T)GCAGCC	1081	bp
2	ACAACCCCC(-:C)TCCCACAG	1149	bp
3	TGCGGAGGGG(A:G)GACCTG	1186	bp
4	AGGT(CAAGGCCAGGT:-)CGAGG	1210	bp

POLYMORPHISMS INSULIN-IGF2 - CONTIG C4 (figure 6)

5	CCC(C:A)CCCC(A:C)CGCCGC	438	bp
6	CCC(C:A)CCCC(A:C)CGCCGC	443	bp
7	CGCCGCAGCA(G:A)GCCG	455	bp
8	GCTTATGG(G:A)GCCGGG	503	bp
9	CACGGC(T:C)TC(G:A)GAGCA	525	bp
10	CACGGC(T:C)TC(G:A)GAGCA	528	bp
11	GTCTGC(A:G)GGCAGGTG	571	bp
12	CAAGCCCGG(G:T)CGGTT	636	bp
13	ACCTC(A:G)AGGCCCCCA	710	bp
14	GC(C:T)GGGCCCAGCCGC	867	bp
15	ACCAGCTG(C:T)GTTCCC	903	bp
16	GGC(C:G)CTCTGGGCGCC	1148	bp
17	GGGGG(C:T)GTCCCGGGA	1305	bp

SUBSTITUTE SHEET (RULE 26)

FIGURE 10, CONTD.

18	GCGGT(C:T)GGGGGAGTT	1320 bp
19	CGCCC(C:T)GGTCCCGCT	1400 bp
20	TCCC(G:A)TCTGCCGGCC	1519 bp
21	GA(T:A)GCCCCATCCCCC	1547 bp
22	GG(C:T)GGCTGCTGCGGC	1607 bp
23	TGGCTGC(G:A)GTCTGGG	2222 bp

POLYMORPHISMES IN CODING REGION - CONTIG C10 (figure 6)

24	GCGCA(G:T)TGATTGGCA	341 bp
25	CGCCCCCCCC(-:C)(G:C)GG	2247 bp
26	CGCCCCCCCC(-:C)(G:C)GG	2248 bp
27	GCAGCCGGCTC(C:T)TGG	2257 bp
28	GTTGTTG(C:T)TCTGGGA	2413 bp

MICROSATELLITES

29 *PIGQTL1*: $(AT)^{11}$ 112 to 133 bp Contig 57

30 *PIGQTL2*: $(GT)^{8}$GCACGCGTGTGCCGTGTGTAC$(GT)^{17}$ 1074 to 1144 bp Contig 95

31 *PIGQTL3*: $(CA)^{19}$ 223 to 260 bp Contig 105

SUBSTITUTE SHEET (RULE 26)